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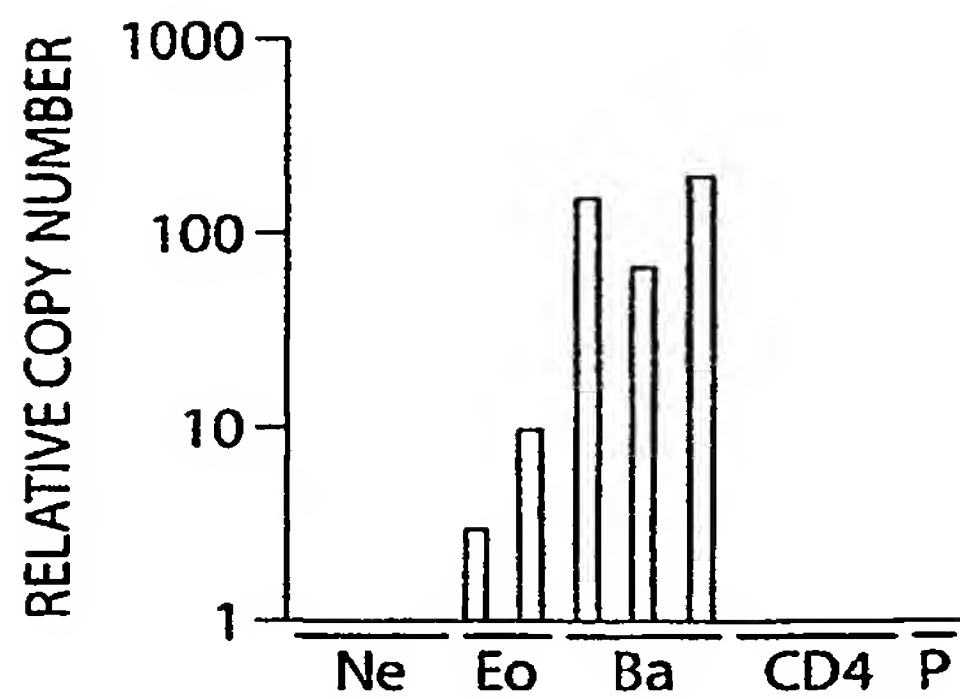


Fig. 1A

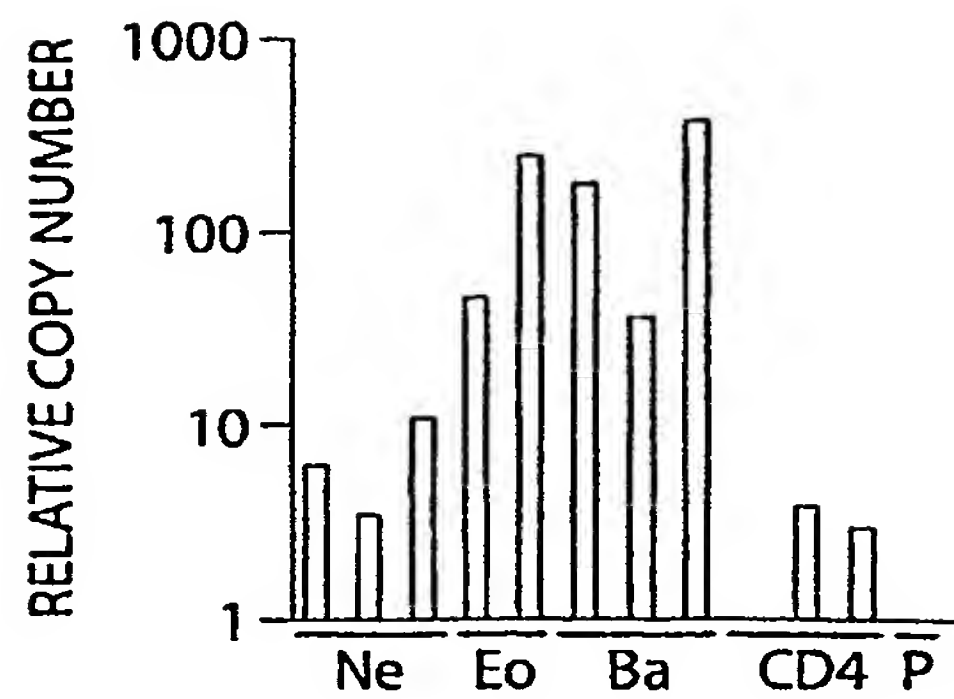


Fig. 1B

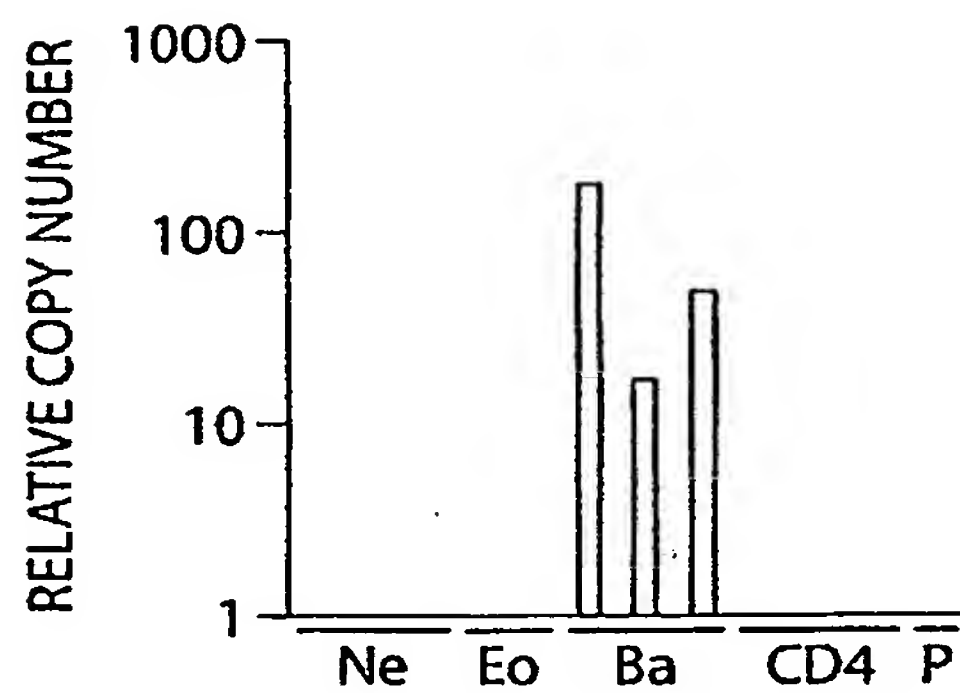


Fig. 1C

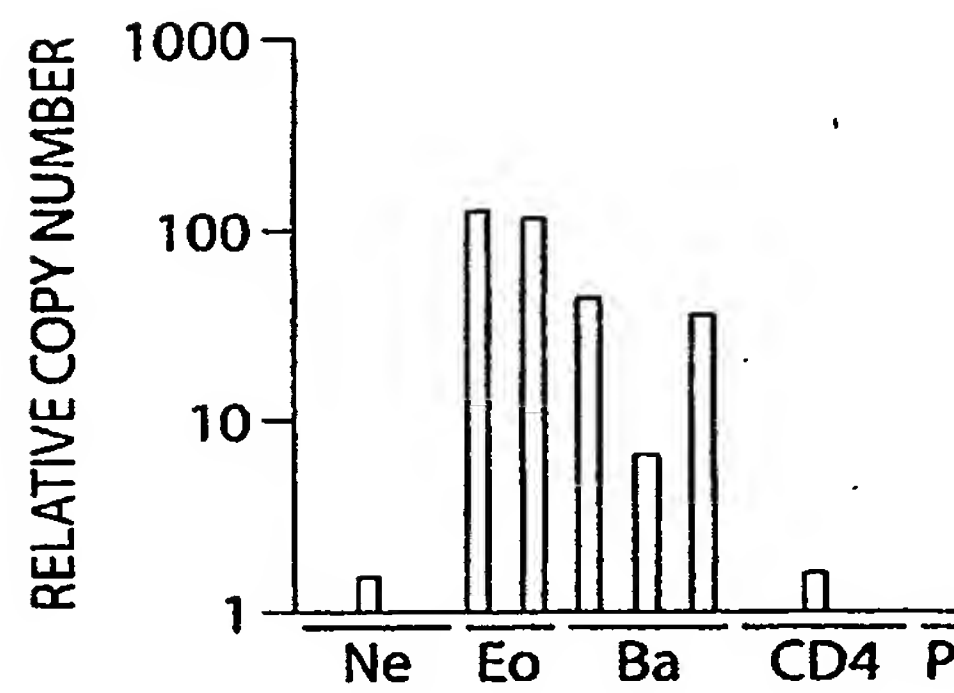


Fig. 1D

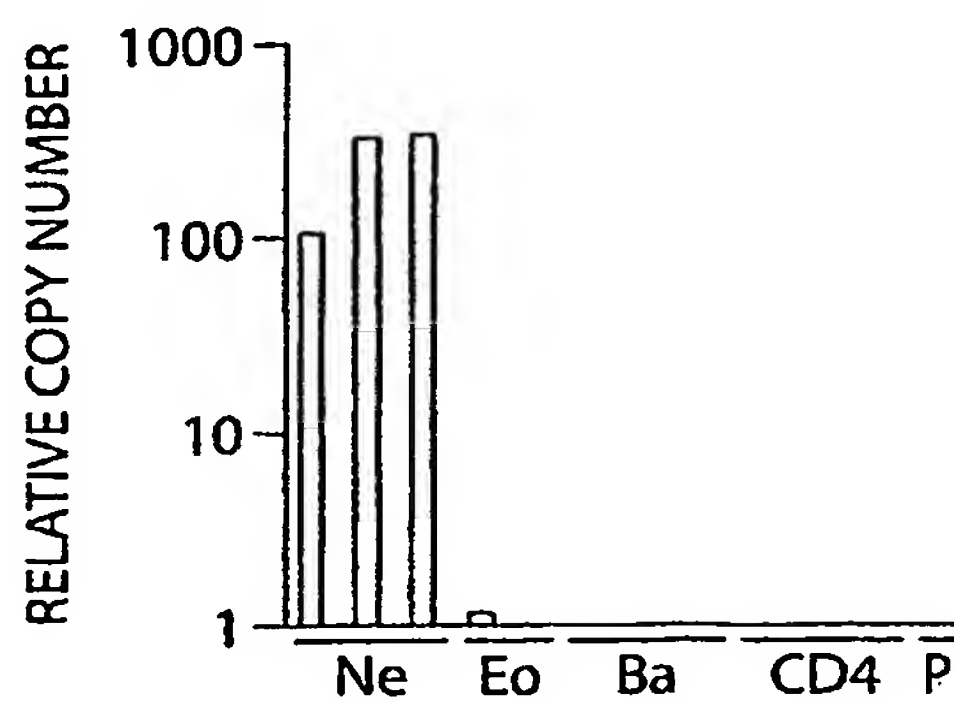


Fig. 1E

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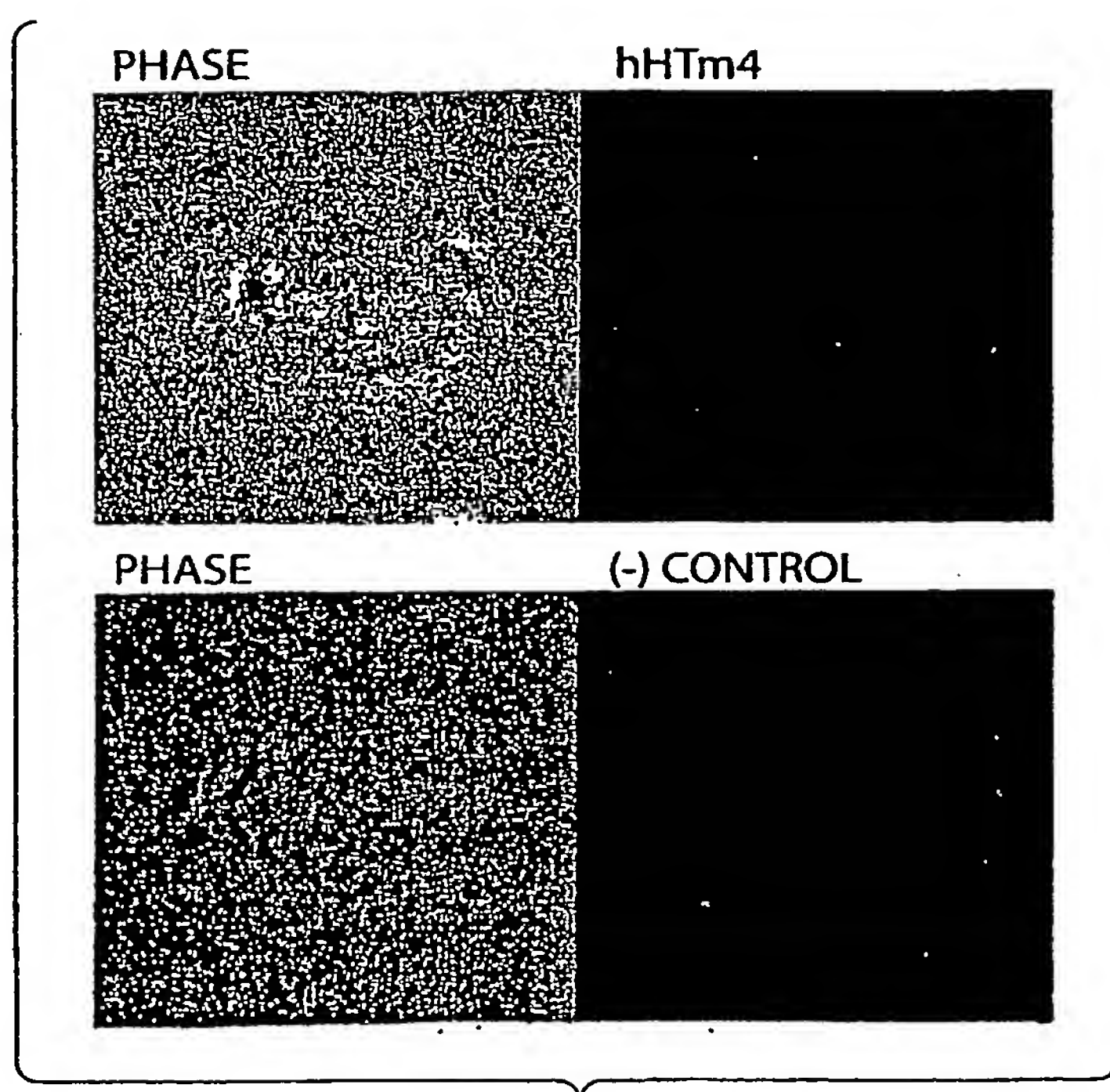


Fig. 2

Figure 3. Granulocyte subtype-specific transcripts for ion channels and receptors

<i>Ion Channels</i>												<i>Gene Functions</i>	
Transcript (Accession #, GenBank)	Cell-type ^a	MC	Ba	Eo	Ne	PI	CD4	CD8	CD14	CD19	Fb	TC ^b	
<u>Ca²⁺ channel type A1 D (BE550599)</u>	Ba, Eo	0.1	1.7	1.5	0.4	0.0	0.3	0.1	0.0	0.3	0.0	0	facilitates uptake of the metalloids arsenite and antimonite
<u>aquaporin 9 (NM_020980) 602914</u>	Ne	0.7	0.1	0.4	137.4	0.4	0.9	0.1	8.6	0.1	0.2	7	
<u>K⁺ channel Kir 1.3 (U73191) 600359</u>	Ne	0.9	0.2	0.4	99.5	0.7	0.2	0.0	0.8	0.0	0.0	5	Andersen syndrome (170390) and Bartter syndrome (241200)
<u>K⁺ channel Kir 2.1 (AF153820) 600681</u>	Ne	0.7	3.8	5.3	40.7	0.4	0.2	0.5	1.5	0.7	1.1	6	Andersen syndrome (170390) and Bartter syndrome (241200)
<i>GPCR</i>													
<u>histamine H₄ R (AF312230) 606792</u>	Ba	0.7	34.2	9.4	0.7	0.4	0.8	0.5	0.6	0.0	0.1	0	expression of HRH4 conferred sensitivity
<u>PGE₂ R type 3a2 (X83858) 176806</u>	Ba	0.8	10.3	0.1	0.7	0.6	0.3	0.2	0.2	0.5	1.7	0	signaling pathways
<u>C3a R (U62027) 605246</u>	Ba, Eo	11.8	55.7	39.4	2.0	1.6	1.6	1.5	3.0	0.6	0.5	3	anaphylatoxin receptor
<u>CCR3 (NM_001837) 601268</u>	Ba, Eo	0.6	117.4	90.9	24.9	0.2	0.5	0.4	0.2	0.2	0.4	0	importance for eosinophil responses
<u>CRTH2 (NM_004778) 604837</u>	Ba, Eo	1.1	26.0	38.2	2.0	0.8	1.4	1.0	1.2	0.9	0.5	0	mediate signals to the interior of the cell via activation of heterotrimeric G proteins
<u>EMR-1 (NM_001974) 600493</u>	Ba, Eo	0.8	33.5	90.9	4.2	3.4	1.7	0.8	7.1	1.6	0.5	1	Probably involved in cellular response to a hormone
<u>adenosine A₃ R (NM_000677) 600445</u>	Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	0	cardioprotective function
<u>P2Y2 purinergic R (NM_002564) 600041</u>	Eo	0.1	0.1	5.5	0.1	0.2	0.1	0.3	1.2	0.2	0.1	0	P2RY2 may participate in control of the cell cycle of endometrial carcinoma cells
<u>GPR 105 purinergic R (NM_014879)</u>	Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	2	GPR105 is a G-protein-coupled receptor identifying a quiescent, primitive population of hematopoietic cells restricted to bone marrow; GPR105 might play an important role in peripheral and neuroimmune function
<u>GPR, Edg-4 (AF011466) 605110</u>	Eo, Ne	1.3	2.8	15.9	24.2	0.1	3.6	5.0	3.8	1.9	0.9	2	edg-4 mrna was expressed in mouse islets; edg-4 (lpa2) r is a distinctive functional marker for ovarian carcinoma, and is expressed both as the wild-type and a carboxyl-terminally extended gain-of-function mutant.
<u>PAR1-like GPR43 (NM_005306)</u>	Eo, Ne	0.3	0.7	12.4	35.2	0.8	0.1	0.1	0.7	0.4	0.1	0	the highest levels of gpr43 were

Fig. 3A

<u>603823</u>										
<u>C5a R (NM_001736) 113995</u>										
Ne	2.3	21.6	13.6	92.6	2.3	1.2	0.5	25.6	1.0	0.4 5
found in immune cells: gpr43 is highly restricted in hematopoietic tissues receptor for the chemotactic and inflammatory peptide anaphylatoxin c5a. this receptor stimulates chemotaxis, granule enzyme release and superoxide anion production.										
<u>CXCR1 IL-8R (NM_000634) 146929</u>										
Ne	0.2	4.3	0.3	83.4	0.4	0.3	0.2	0.2	0.1	0.1 0
receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to mgsa (gro) with a low affinity.										
<u>CXCR2 IL-8R (NM_001557)</u>										
Ne	0.2	1.1	1.5	112.1	2.7	0.3	0.8	0.7	0.6	0.0 1
receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to gro/mgsa and nap-2 also with a high affinity.										
<u>formyl peptide R 1 (NM_002029) 136537</u>										
Ne	2.8	23.5	8.8	282.9	3.6	1.3	0.7	62.6	1.1	0.5 0
HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED										

Fig. 3B

Fig. 3C												VIA A G-PROTEIN THAT ACTIVATES PHOSPHATIDYLINOSITOL- CALCIUM SECOND MESSENGER SYSTEM. likely FPR2, mediates superoxide production at high concentrations of fMLF C5L2 is an anaphylatoxin- binding protein with unique ligand binding and signaling properties GPR86 proved to be a G(i)- coupled receptor displaying a high affinity for ADP, similar to the P2Y(12) receptor and can therefore be tentatively called P2Y(13) PAR2 plays a key role in chronic joint inflammation
formyl peptide R 2 (U81501)	Ne	0.4	0.5	0.6	75.5	0.1	1.0	0.6	6.0	0.8	0.1	5
GPR77 (NM_018485)	Ne	0.1	0.9	0.8	3.4	0.0	0.3	0.2	1.0	0.1	0.3	2
GPR86 purinergic R (NM_023914)	Ne	0.3	0.2	17.9	88.2	1.9	0.1	0.2	12.3	0.6	0.0	1
PAR2 (BE965369) 600933	Ne	0.1	0.3	2.2	36.2	0.1	0.7	0.1	1.6	0.4	1.2	15
Other Receptors Fcε RI α (BC005912) 147138	Ba	19.4	219.0	4.6	5.5	1.4	5.1	0.8	1.4	0.4	0.2	0
HTm4 (L35848) 606498	Ba	0.6	133.1	6.9	3.5	0.2	0.5	0.4	0.1	0.2	0.0	1
IL-3 R (NM_002183) 308385	Ba	0.6	52.6	2.0	0.7	0.2	0.3	0.2	0.7	0.1	0.1	0
CD244 NK cell R NM_016382 605554	Ba, Eo	0.3	56.0	16.5	1.2	0.1	0.4	3.5	5.2	1.1	0.1	0
fibroblast growth factor R 2 (NM_022969) 176943	Ba, Eo	0.1	27.9	12.1	0.2	0.1	0.1	0.2	0.1	0.1	1.0	17
IL-5R α (M75914) 147851	Ba, Eo	0.9	20.5	30.4	0.6	0.1	0.1	0.1	0.1	0.2	0.1	0
Siglec 8 (NM_014442) 605639	Eo	1.8	0.3	17.4	0.4	0.3	0.2	0.1	0.2	0.5	0.2	0
CD117 c-KIT (NM_000222) 164920	MC	89.0	7.2	4.2	1.2	0.8	0.2	0.5	0.1	0.1	0.5	15
SiglecB D86358 604405	MC	5.6	0.2	0.0	0.2	0.5	0.0	0.0	0.0	0.4	0.0	0
Fcε RIβ (NM_000139) 147138 low density lipoprotein R	MC, Ba MC, Ba	22.3 20.7	44.3 20.4	0.4 1.3	0.6 1.8	1.6 2.3	0.5 2.1	0.2 3.4	0.0 3.5	0.3 0.8	0.1 6.3	0 34

<u>(NM_000527) 606945</u> <u>TRK neurotrophin R (NM_002529)</u> <u>191315</u>	MC, Ba	4.6	7.3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0	participates in the primary signal transduction mechanism of NGF; is also an immunoregulatory cytokine acting on monocytes his gene is mainly expressed in small intestine, colon, testis, and leukocytes
<u>butyrophilin like R (AK025267)</u>	Ne	1.1	1.7	1.5	6.9	1.5	1.7	1.6	0.9	1.5	1.3	1	1	<u>Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Contributes to the induction of noncytotoxic TNF effects including anti-viral state and activation of the acid sphingomyelinase.</u>
<u>CD120a, TNF-R-1 (NM_001065)</u> <u>191190</u>	Ne	1.7	1.2	7.8	74.7	1.3	2.2	5.9	17.4	0.6	16	35	35	<u>Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both. The secreted</u>
<u>CD95, Fas, APO-1 (AA164751) 134637</u>	Ne	1.4	10.9	7.3	50.4	1.3	5.6	4.8	3.6	2.6	9.7	7	7	

Fig. 3D

<u>decoy R1, TRAILR3 (AF012536)</u> <u>603613</u> FcγR IIC2 (U90939) FcγR IIC3 (U90940) FcγR III (J04162) <u>146740</u>	Ne	0.1	1.5	7.7	78.7	0.5	0.2	0.1	0.7	0.1	0.6	0	<u>isoforms 2 to 6 block apoptosis</u> <u>(in vitro).</u> does not induce apoptosis.
	Ne	1.5	2.4	7.8	59.9	0.3	0.2	0.1	7.2	2.3	0.2	2	
	Ne	2.4	10.7	10.0	84.3	3.0	1.4	0.6	14.0	7.2	1.0	5	
	Ne	0.7	1.6	1.9	199.6	6.6	1.3	1.3	2.2	2.6	0.1	4	
G-CSF R (NM_0007601) <u>138971</u> IL-13 R (U81379) <u>308385</u>	Ne	0.1	0.4	1.6	163.6	0.2	0.8	0.2	25.5	0.1	0.2	3	failure of the patient's neutrophils to express Fc receptor III was associated with SLE inhibits cell proliferation and survival in response to CSF3 romotes the proliferation and differentiation of hematopoietic cells
	Ne	0.3	0.2	2.0	14.1	0.4	0.4	0.3	2.9	1.3	1.3	0	
IL-1R, type II (NM_004633) <u>147811</u>	Ne	0.1	0.1	0.1	53.5	0.2	0.4	0.1	0.2	0.0	0.0	3	type II receptor inhibits IL1 activity by acting as a decoy target for IL1 IGFs may elicit a myogenic event which may be a key mechanism in the etiology of breast and ovarian cancer Mutation in either MPRD or MPRI might result in a clinical disorder resembling a mucopolidosis Eosinophils may be activated through L1R7 for release of eosinophil-derived neurotoxin that TLR2-TLR1 heterodimers mediated the strongest cell activation TLR2 is a molecular link between microbial products, apoptosis, and host defense mechanisms immunostimulatory activity
IGFR 1 (NM_000875) <u>147370</u>	Ne	0.3	3.5	5.0	17.4	1.6	0.1	2.8	2.4	2.0	3.5	3	
IGFR 2 (NM_000876) <u>147280</u>	Ne	4.6	0.9	5.4	85.3	1.7	2.9	8.7	8.4	4.8	15	32	Eosinophils may be activated through L1R7 for release of eosinophil-derived neurotoxin that TLR2-TLR1 heterodimers mediated the strongest cell activation TLR2 is a molecular link between microbial products, apoptosis, and host defense mechanisms immunostimulatory activity
leukocyte immunoglobulin-like R A2 (NM_006866) <u>604812</u>	Ne	0.5	5.8	4.3	41.2	1.8	0.0	0.1	11.6	0.5	0.1	2	
Toll-like R 1 (AL050262) <u>601194</u>	Ne	0.6	0.3	1.2	31.5	1.6	0.8	0.7	3.0	1.5	0.3	0	Eosinophils may be activated through L1R7 for release of eosinophil-derived neurotoxin that TLR2-TLR1 heterodimers mediated the strongest cell activation TLR2 is a molecular link between microbial products, apoptosis, and host defense mechanisms immunostimulatory activity
Toll-like R 2 (NM_003264) <u>603028</u>	Ne	0.9	6.0	1.3	83.8	1.6	1.3	0.1	26.3	0.9	0.4	0	
Toll-like R 6 (NM_006068)	Ne	0.5	1.0	0.9	8.8	0.1	0.9	0.9	2.1	1.2	0.6	0	

a. Cell-type specificity was obtained by comparing the "normalized AD" levels of each gene in mast cells (MC; average of 2 experiments), basophils (Ba; average of 3 experiments), eosinophils (Eo; average of 4 experiments), neutrophils (Ne; average of 4 experiments), platelets (Pl), CD4⁺ cells (CD4), CD8⁺ cells (CD8), CD14⁺ cells (CD14), CD19⁺ cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb).

Fig. 3E

	CB cultured		cultured		Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19
	MCs	Basophils	basophils	Eosinophils							
Spink5	21	17	11	22	16	30	15	28	36	129	104
chymase human	1221	47	65	45	12	101	62	108	59	104	45
tryptase alpha	21179	212	40	33	25	184	139	104	17	52	39
tryptase beta	25414	195	113	49	28	152	10	122	113	93	6
tryptase delta	349	45	6	23	55	74	113	11	10	42	11
tryptase gamma	654	56	19	38	78	28	24	81	230	142	83
TRPV2	129	37	15	97	99	259	137	133	67	97	110
ANKTM1_	28	28	8	38	30	96	18	14	46	11	28
Cannabinoid receptor type 1	50	41	14	47	36	27	61	41	56	18	54
Cannabinoid receptor type 2	160	369	226	578	177	271	530	324	232	212	421

Fig. 4A

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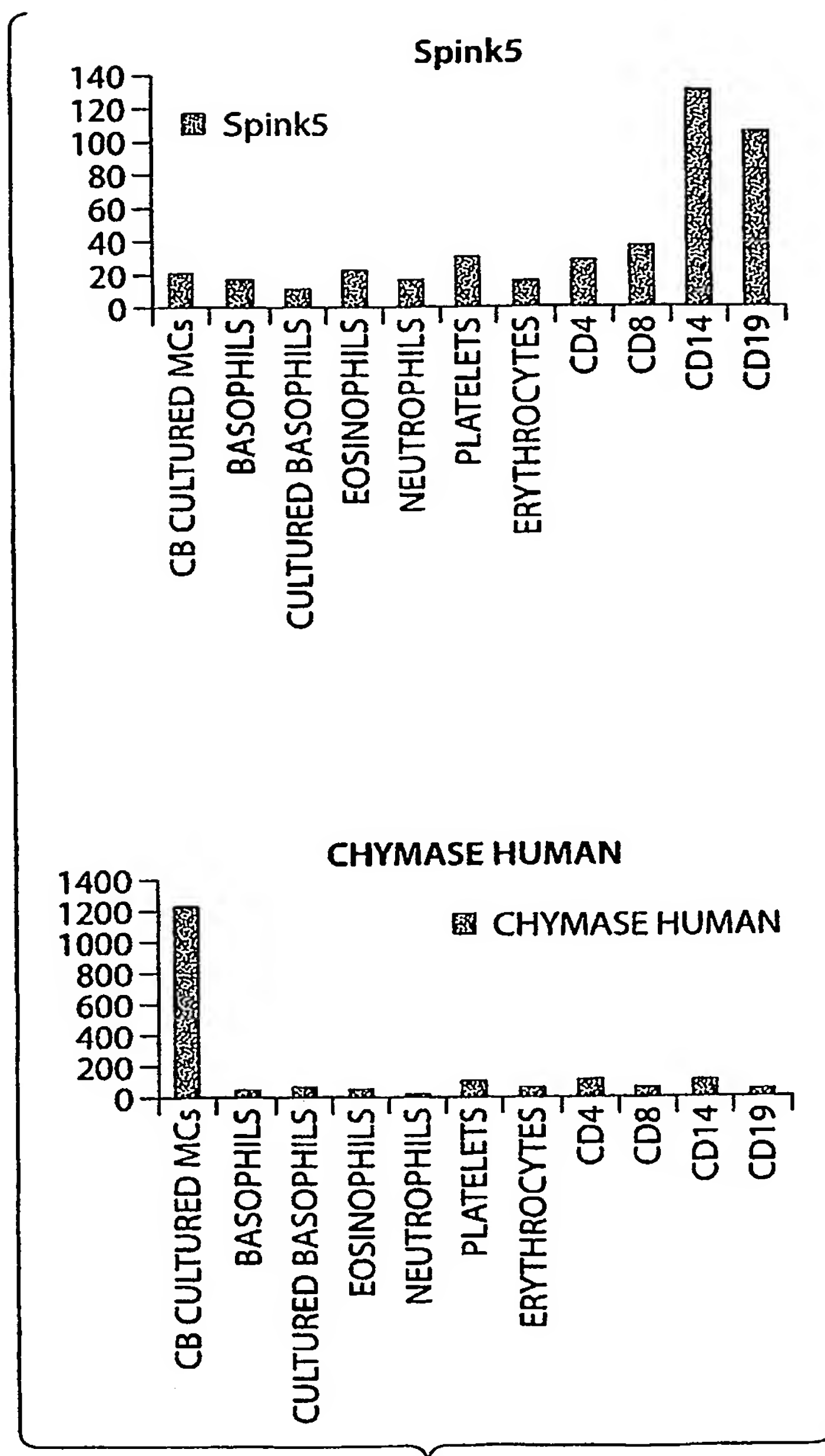


Fig. 4B

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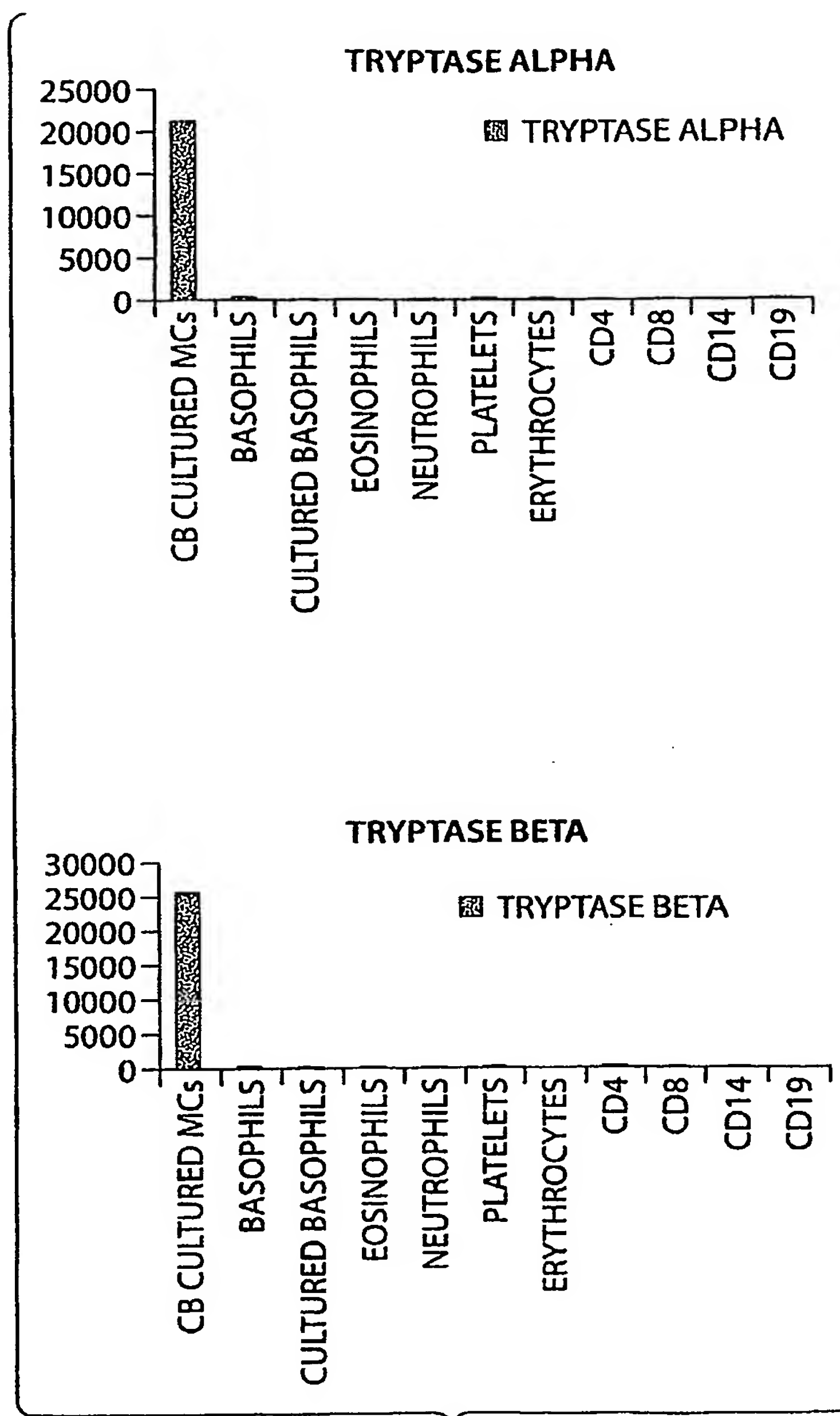


Fig. 4C

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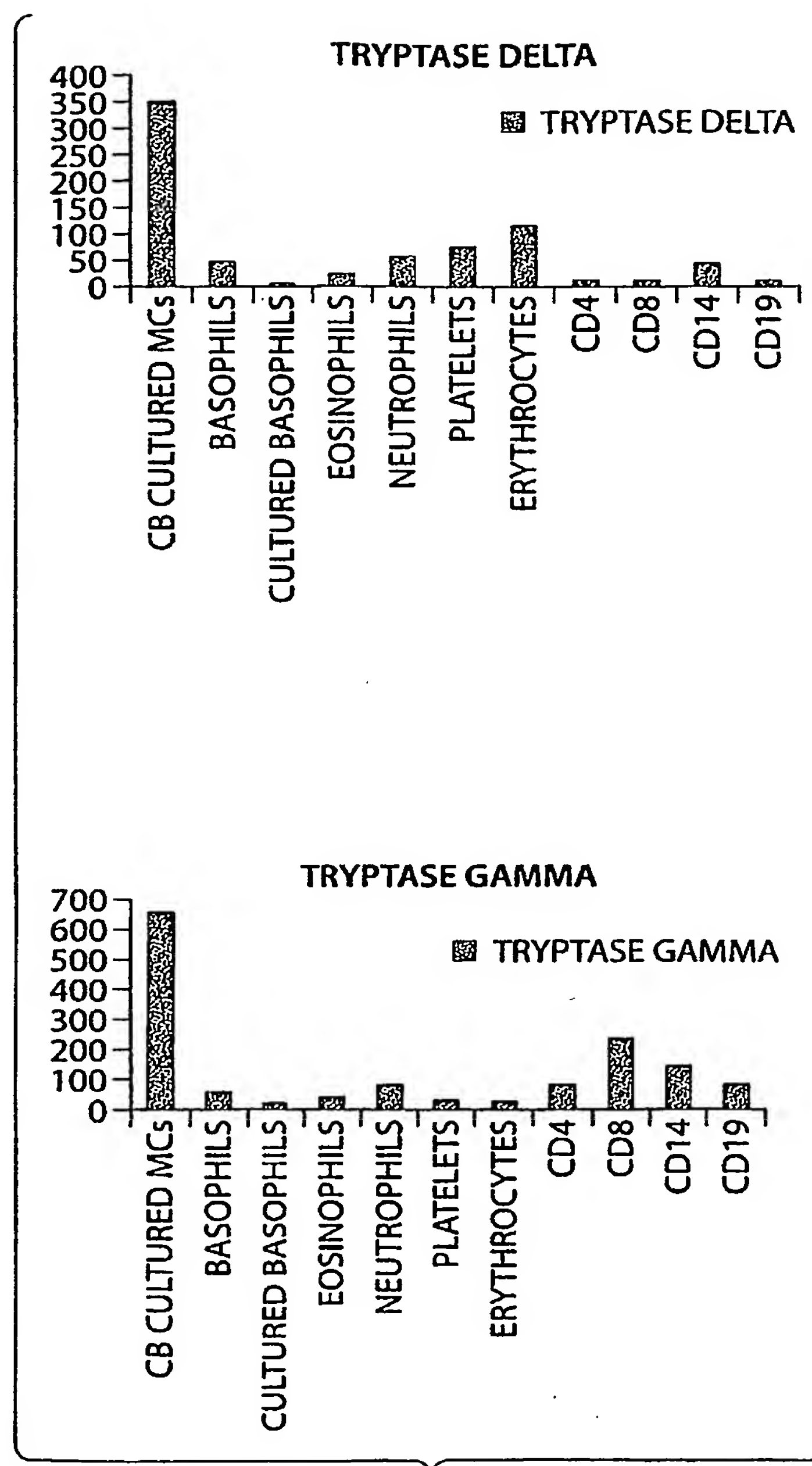


Fig. 4D

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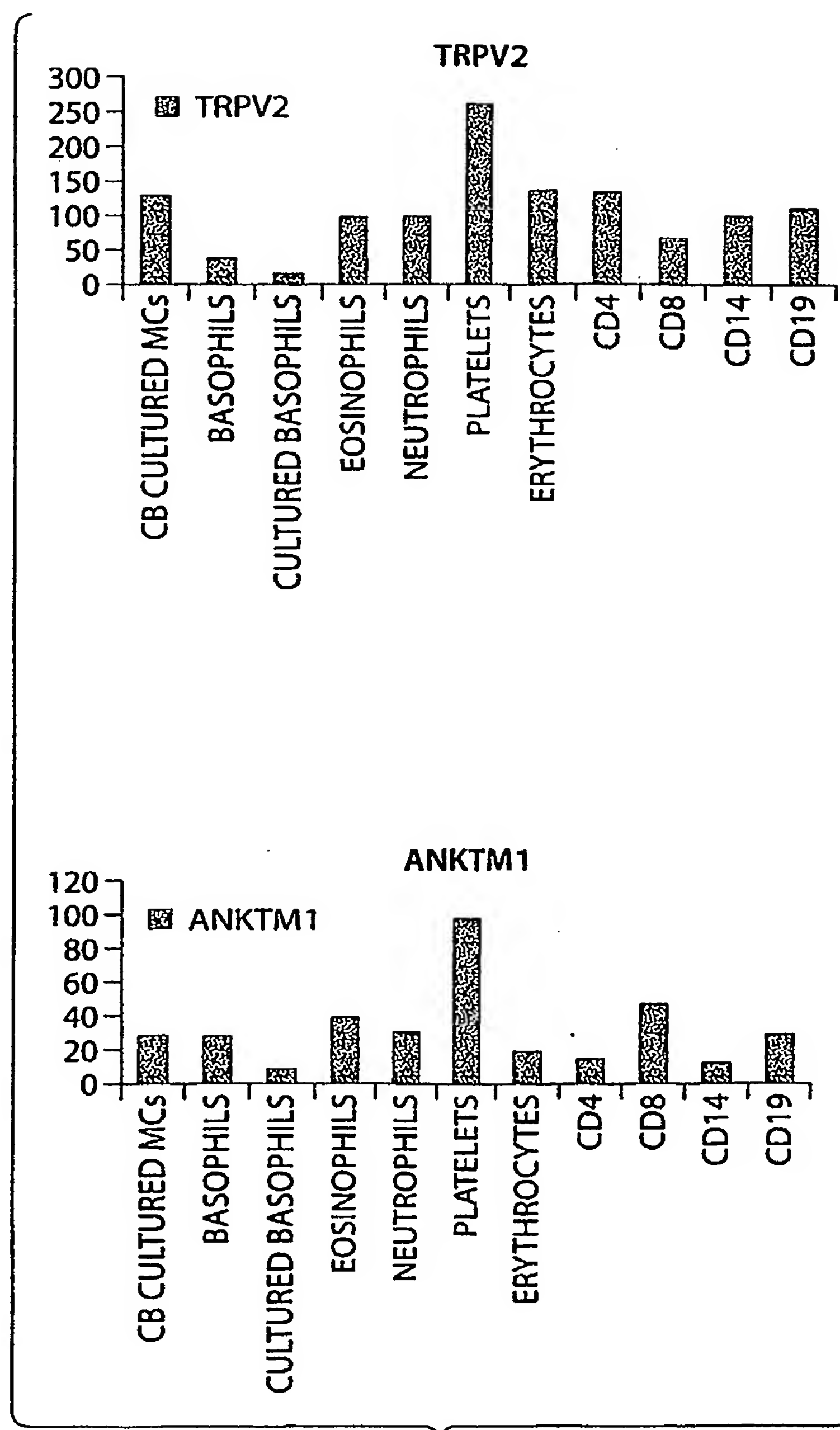


Fig. 4E

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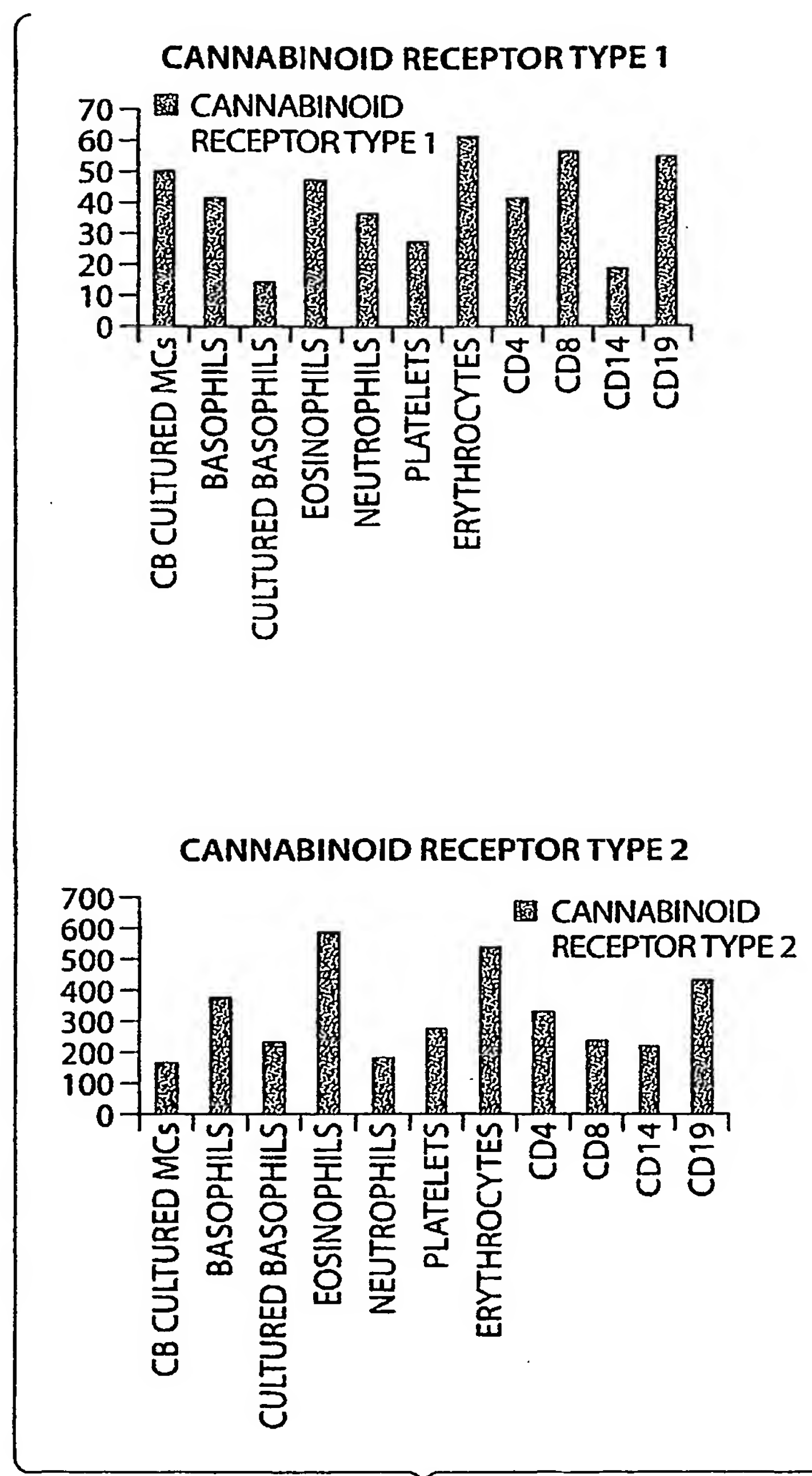


Fig. 4F

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CB cultured MCs	Basophils	cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19
86	28	39	26	37	125	46	103	95	85	28
4	45	1004	59	84	18	68	31	68	451	13
165	84	51	258	1261	31	42	13	18	1105	125
375	780	227	1755	4237	199	375	286	58	2963	214
49	614	384	461	3269	146	318	8	9	1247	52
28	50	45	154	389	120	148	127	35	539	86
7	58	34	18	23	13	106	14	286	68	204
22	17	21	27	28	35	11	28	110	88	111
30	54	134	66	61	149	95	39	247	147	271
35	138	81	88	93	191	132	57	257	21	267
24	31	23	21	21	53	27	33	135	19	173
139	140	85	157	144	280	210	35	239	152	196
11	45	41	50	41	88	15	19	72	77	85
41	43	31	20	52	31	121	96	163	26	193
27	83	24	41	49	61	239	92	323	56	72
68	89	41	51	95	75	97	76	169	36	196
144	621	83	1334	2386	107	146	145	52	2154	99
18	14	5	28	37	86	12	13	14	32	23

Fig. 5A

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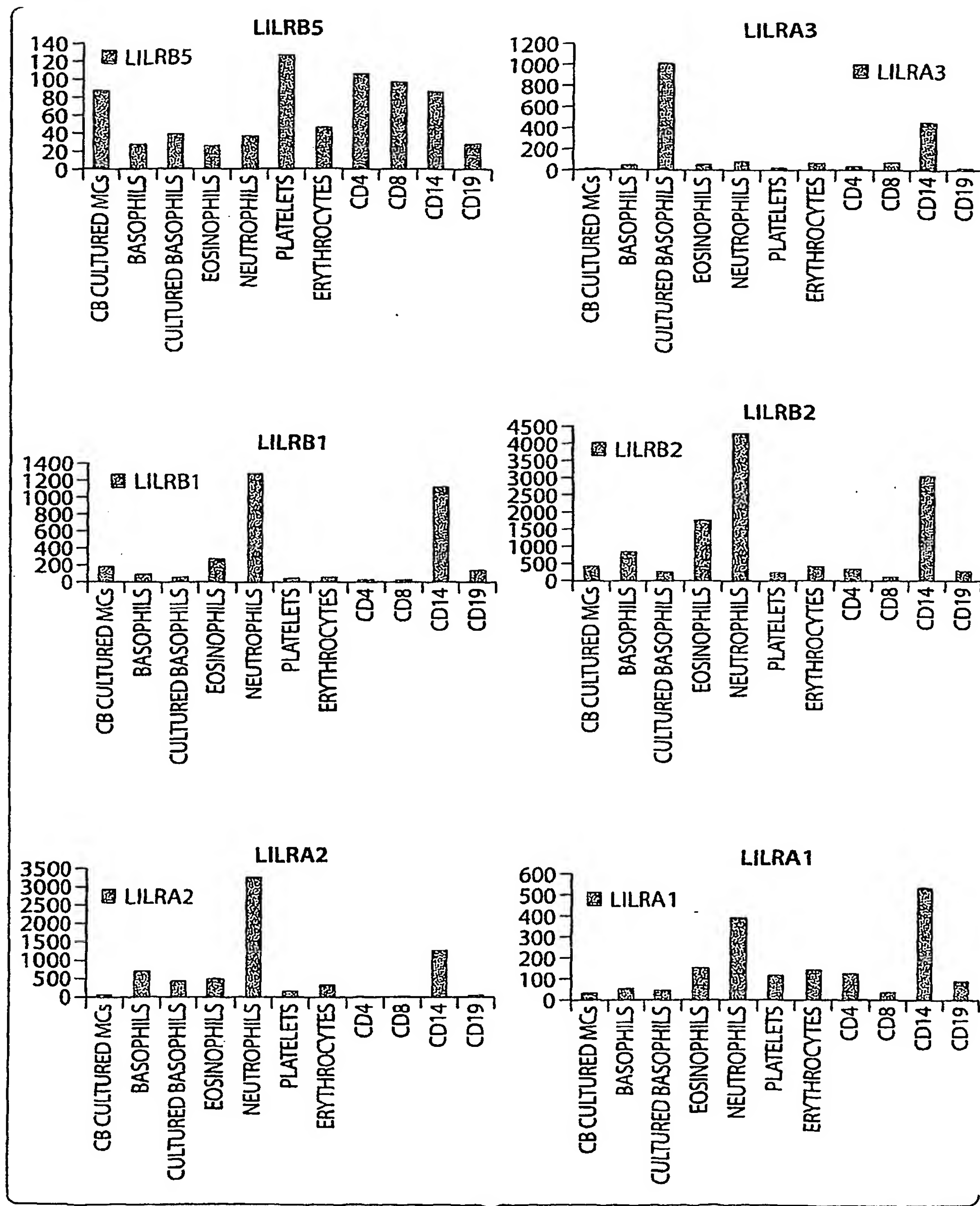


Fig. 5B

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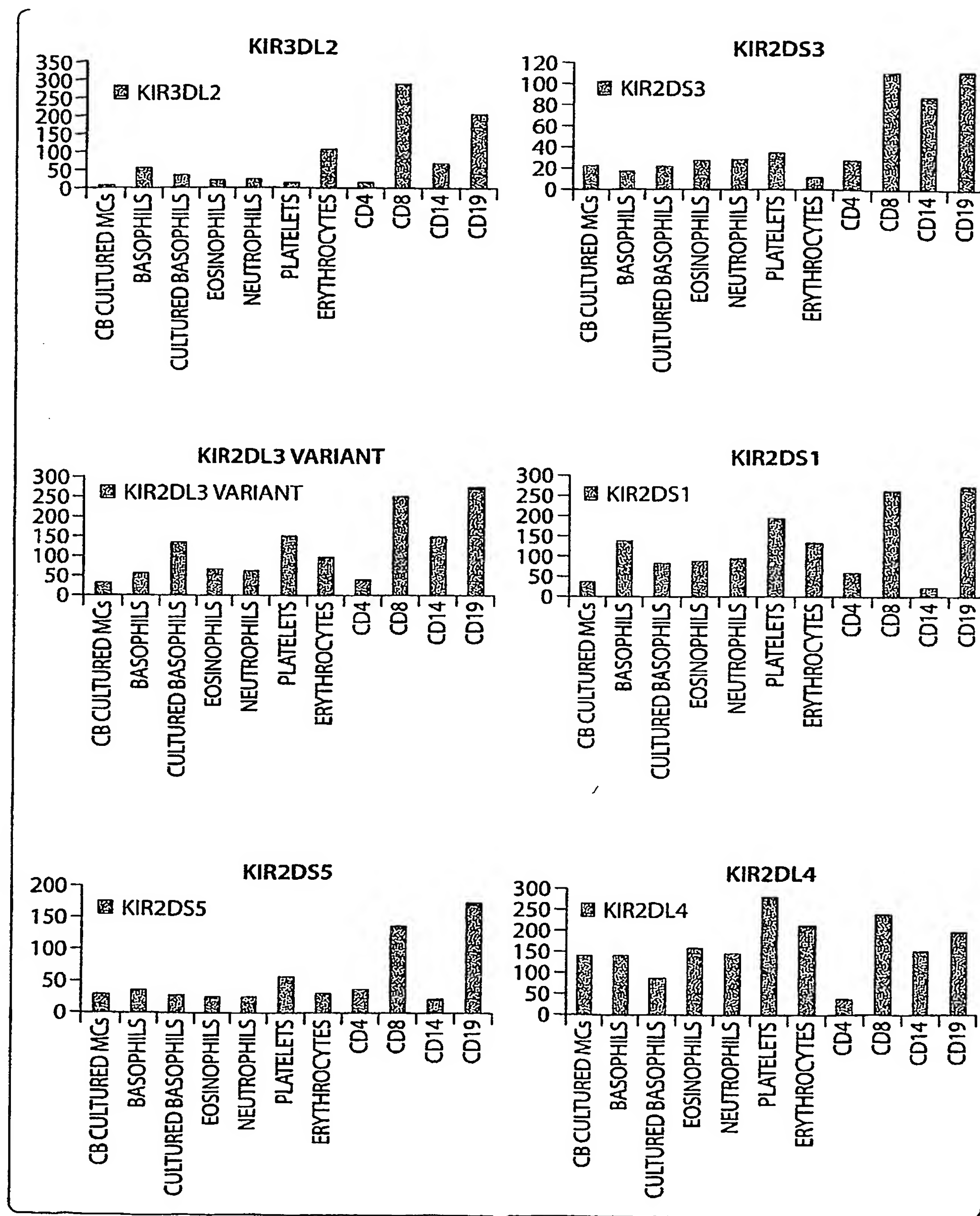


Fig. 5C

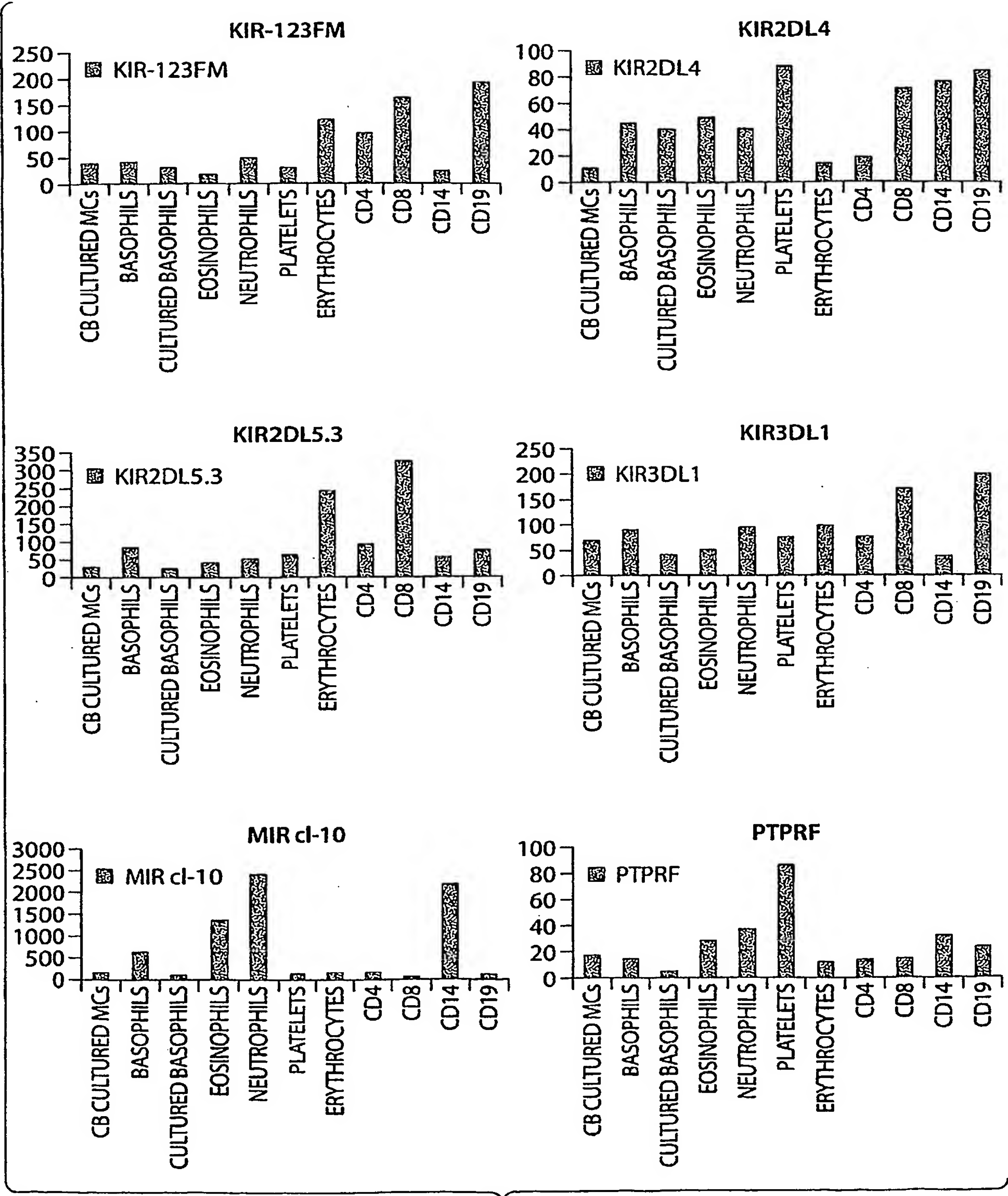


Fig. 5D

Table E1. The complete list of granulocyte subtype-selective transcripts. Selectivity index (S.I.) was calculated by comparing the "normalized AD" level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (Pl), CD4⁺ cells, CD8⁺ cells, CD14⁺ cells, CD19⁺ cells and nasal polyp-derived cultured fibroblasts (Fb). When the result was accompanied by presence call, it was shown as a bold numeral. Italic numerals show that the raw AD levels were associated with absence call by the GeneChip analysis software. Transcripts having S.I. >3-fold were shown in A-H. Abbreviations used in the table through A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

A. Basophil (Ba)-selective transcripts (1/2).

		MC		cord		blood		lung		MC		Ba1		Ba2		Ba3		Eo		Eo3		Eo4		Ne		Ne3		Ne4		pl		CD4		CD8		CD14		CD19		Fb		Ba.S.I.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
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Fig. 6A-1

MC cord blood	Transcripts	Accession #	Probe set	MC		Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo4		Ne 2	Ne3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba.SI.
				lung	MC.						(small)	(small)										
4.7	2.0	20.8	30.6	25.9	2.1	2.8	3.8	1.7	0.5	1.1	1.3	0.1	0.2	0.1	3.8	0.2	3.2	6.6846				
0.1	0.4	3.7	15.5	24.4	2.0	0.9	2.5	2.3	0.2	0.1	0.7	0.6	1.1	1.5	0.5	0.6	0.7	6.2585				
2.3	1.5	9.8	49.0	34.3	3.7	3.3	4.8	4.2	1.6	1.0	1.9	2.2	4.1	3.0	0.8	2.0	2.6	6.2142				
2.2	1.2	9.9	19.1	16.6	2.3	1.5	3.6	2.5	1.1	1.1	1.9	0.9	1.8	2.0	2.0	1.4	0.8	6.2011				
1.8	0.3	10.7	15.9	6.5	0.9	0.6	1.2	0.9	0.8	0.4	1.1	1.3	1.0	1.3	1.2	1.1	1.7	6.1557				
1.8	3.1	11.0	27.5	15.1	1.6	1.1	1.4	2.1	1.1	1.4	1.3	1.8	1.6	1.1	1.1	0.6	2.9	5.6407				
1.8	1.7	5.9	12.5	11.4	1.0	0.5	1.2	0.5	1.2	1.7	1.2	1.2	0.9	1.0	1.2	1.0	0.4	1.7	5.4082			
6.4	4.9	29.6	47.7	42.3	0.8	0.3	0.4	0.6	0.3	0.0	0.9	1.4	1.0	7.3	3.1	0.9	0.7	1.4	5.3183			
0.9	0.2	12.2	17.0	12.0	3.5	1.7	0.5	0.6	0.1	0.3	0.8	0.4	0.6	1.5	2.6	0.7	1.6	1.3	5.2721			
1.6	3.8	23.9	51.9	43.5	4.6	4.0	7.1	7.3	1.6	2.1	2.5	2.3	1.7	3.7	7.4	3.2	4.7	4.2	5.107			
6.9	3.2	7.2	29.2	58.9	2.8	3.2	5.4	6.3	0.9	1.2	1.8	1.6	1.6	2.2	2.4	2.0	3.5	1.8	4.9129			
2.7	1.8	17.5	38.8	25.8	4.0	6.7	6.2	4.8	1.4	0.9	0.8	1.1	0.2	1.2	1.5	0.6	1.1	1.9	4.8879			
0.0	0.9	4.1	6.1	5.8	0.8	1.4	0.9	1.4	0.6	0.1	0.5	0.2	1.0	0.4	0.2	0.2	0.4	0.3	4.855			
64.1	14.7	105.2	164.9	165.7	3.4	1.4	4.1	2.8	2.1	1.2	4.6	14.0	2.4	0.8	0.9	1.1	0.7	0.2	4.6305			
1.0	0.6	2.4	11.5	17.0	0.3	0.1	0.1	0.0	0.4	0.7	0.9	0.7	0.6	0.3	0.2	0.2	0.5	1.7	4.6103			
2.1	1.1	3.7	11.0	7.8	1.0	0.6	1.5	0.5	1.2	0.3	1.5	0.9	1.1	0.7	0.3	1.0	0.2	0.4	4.5552			
5.2	0.2	3.0	24.1	29.9	2.1	3.0	3.2	3.4	0.3	1.0	0.8	1.3	0.8	0.8	0.8	0.0	0.8	0.9	4.5248			
0.3	0.6	5.3	12.9	12.5	0.4	2.4	4.2	2.0	1.0	0.8	0.7	0.3	1.9	0.5	0.7	2.1	0.2	0.2	4.5061			
0.4	0.0	2.3	7.3	5.5	0.5	0.4	0.6	0.5	0.1	0.1	1.0	0.6	0.7	0.1	0.0	1.0	0.0	0.5	4.4335			
0.1	0.2	7.5	14.3	22.1	2.3	2.0	4.9	3.7	1.2	1.3	1.5	2.5	1.4	0.5	0.2	1.1	0.9	0.8	4.363			

Fig. 6A-2

A. Basophil (Ba)-selective transcripts (2/2).

Probe set	Accession #	Transcripts	MC										20/36									
			cord	MC	Ba1	Ba2	Ba3	EO	EO	EO3	EO4	Ne	Ne3	Ne4	CD4	CD8	CD14	CD19	Fb	Ba.S1		
214651_s_at	U41813.1	class 1 homeoprotein (HOXA9)	0.6	0.6	1.7	63	83	0.3	0.5	0.8	0.5	0.1	0.1	1.0	1.0	0.1	0.3	0.1	0.1	4.3618		
32502_at	AL041124	DKFZp434D0316_s1	1.6	1.9	14.6	22.5	17.4	4.0	2.1	0.7	1.4	1.1	1.0	0.4	2.3	2.5	4.1	2.3	1.8	4.3594		
205373_at	NM_004389.1	catenin (cadherin-associated protein)	0.2	0.1	1.1	3.9	3.2	0.6	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.6	0.2	0.2	4.2308		
219676_at	NM_025231.1	alpha 2	0.3	0.7	2.5	7.3	12.0	0.9	0.2	2.0	1.5	0.2	1.1	2.2	0.6	1.1	1.4	0.3	0.1	4.2135		
213385_at	AK026415.1	beta2-chimaerin	4.7	3.1	8.3	22.9	21.8	1.1	0.8	0.9	1.0	0.2	1.5	1.0	0.1	0.9	1.6	3.3	0.2	4.2131		
214637_at	BG437034	oncostatin M	0.4	0.0	0.9	5.4	4.4	0.2	0.7	0.1	0.7	0.5	1.8	1.1	0.4	0.1	0.1	0.2	0.1	4.1983		
202490_at	AF153419.2	Ikeppa B-associated protein	0.2	0.2	1.3	3.6	2.2	0.4	0.4	0.5	0.1	0.3	0.0	0.0	0.3	0.3	0.5	0.2	0.4	4.1747		
220416_at	NM_024837.1	FLJ21472	4.1	1.5	9.1	9.7	12.2	1.9	3.3	3.0	1.9	0.8	0.6	0.9	0.7	0.6	0.2	0.8	0.3	4.1718		
218318_s_at	NM_016231.1	nemo-like kinase	1.4	1.3	6.2	7.0	7.1	0.8	0.9	0.8	0.6	0.5	1.0	0.1	1.6	1.3	0.9	1.2	1.1	4.1558		
215201_at	AW166925	FLJ14135 fs; clone MAMMA1002728	0.1	0.1	2.1	3.5	5.1	0.5	0.7	0.8	0.9	0.0	0.1	0.1	0.5	0.3	0.8	0.4	0.5	4.1491		
222303_at	AV700891	ETS2 intronic transcript 1 mRNA	0.6	1.4	31.1	86.8	63.8	3.6	2.2	2.9	3.2	10.8	10.5	19.0	1.2	0.7	0.7	0.3	0.8	4.0555		
201664_at	AL136877.1	DKFZp434F205	2.8	5.0	17.3	27.7	31.8	4.4	5.3	9.1	8.3	4.3	3.9	5.5	0.1	4.8	4.2	4.1	4.8	3.8471		
210252_s_at	AB002356.1	MAP-kinase activating death domain	5.6	4.6	12.7	35.0	40.7	6.2	6.1	7.0	8.3	2.2	1.3	3.3	5.2	2.7	5.4	3.5	1.1	3.8424		
201328_at	AL575509	vets avian erythroblastosis virus E26	1.7	0.1	18.4	34.7	50.7	2.8	1.6	1.7	1.8	6.4	9.9	8.9	0.5	0.9	1.0	4.4	0.1	3.8075		
218392_x_at	NM_022754	onco gene homolog 2	1.2	1.0	3.5	7.5	7.4	1.4	1.0	2.7	1.5	1.0	0.6	0.9	0.9	1.4	0.4	0.7	0.5	3.7693		
205046_at	NM_001813.1	FLJ12876	0.0	0.3	1.5	8.1	13.1	1.7	0.5	1.9	1.2	0.5	1.3	1.0	1.1	1.5	0.9	1.0	0.4	3.7324		
221170_at	AF312230.1	FLJ14150 fs; clone MAMMA1003026	0.6	0.8	35.9	34.2	32.5	7.8	11.9	8.7	9.3	0.2	0.8	1.0	0.4	0.8	0.5	0.6	0.0	3.6719		
201663_s_at	NM_005496.1	histamine H4 receptor	2.2	4.3	17.6	15.1	18.1	3.4	6.6	4.9	4.2	4.0	3.7	2.7	1.7	4.1	2.9	1.7	3.7	3.6472		
208933_s_at	AI659005	chromosome-associated polypeptide C	11.8	4.9	26.7	28.3	28.2	5.9	6.6	10.1	4.8	3.8	4.5	5.5	4.3	7.6	7.4	7.2	4.3	3.6311		
209710_at	AL563460	lectin, galactoside-binding, soluble, 8	50.4	38.9	141.1	189.2	154.7	4.4	1.3	3.8	3.1	0.7	1.2	10.8	2.5	0.7	0.9	0.3	0.1	3.6251		
205769_at	NM_003645.1	GATA-binding protein 2	3.3	2.5	7.0	16.2	9.2	0.3	0.3	0.3	0.5	0.1	0.4	0.3	0.2	0.4	0.7	0.1	0.3	3.5389		
209409_at	D86962.1	long-chain 1 (FACVL1)	8.4	2.6	12.5	38.0	33.1	4.9	4.2	12.3	10.4	1.7	1.7	2.1	1.4	0.4	0.7	1.5	0.4	3.4907		
38398_at	AB002356	KIAA0207	5.5	4.1	13.8	24.6	29.8	6.1	6.4	5.6	7.0	3.0	3.2	3.3	5.1	3.3	5.3	3.7	4.4	3.4534		
205899_at	NM_003914.1	KIAA0358	5.6	3.6	16.2	20.6	10.5	0.1	0.6	0.9	0.1	1.6	0.1	0.8	1.9	0.7	0.1	0.1	0.3	3.3824		
218150_at	NM_012097.1	cyclin A1	8.2	5.3	37.6	56.6	54.6	9.1	8.6	14.0	12.1	3.9	5.0	7.7	3.8	8.3	8.1	14.5	9.9	3.3745		
213097_s_at	AI338837	ADP-ribosylation factor-like 5	2.1	1.8	8.4	13.4	16.7	4.8	2.1	4.8	3.7	1.8	1.2	1.2	0.3	3.4	3.7	2.3	3.3	3.3672		
208158_s_at	NM_018030.1	zinc-binding protein-related protein	1.2	2.3	8.8	18.0	15.3	0.6	0.8	1.6	1.4	1.5	2.3	2.7	2.0	0.2	0.7	1.3	0.5	3.342		
210109_at	AF191492.1	oxysterol-binding protein	1.2	0.7	3.6	6.4	4.2	1.2	1.6	1.0	0.3	0.6	1.1	1.7	0.6	1.3	0.5	1.4	0.6	3.2977		
220918_at	NM_025143.1	nasopharyngeal carcinoma associated gene protein-8	1.0	1.1	26.1	37.3	26.2	6.2	6.5	14.1	11.3	3.3	2.5	2.0	1.1	0.9	0.9	3.5	1.1	3.2902		
209359_x_at	L34598.1	aml1 (acute myeloid leukemia 1)	1.2	0.1	3.1	7.2	7.1	2.5	1.6	1.6	1.1	0.2	1.0	1.4	0.7	0.7	1.0	0.8	0.6	3.2789		
208107_s_at	NM_030941.1	onco gene	3.6	7.6	7.8	30.6	20.1	1.6	2.3	2.7	0.8	0.6	0.2	1.5	0.2	0.1	0.3	0.2	0.1	3.2356		
212412_at	AV715767	exonuclease NEF-sp	18.2	16.2	41.3	72.5	67.3	7.7	7.7	16.3	11.6	6.4	6.3	9.1	3.7	3.1	4.1	8.0	3.3	3.2017		
215215_s_at	AC004381	DKFZp564A072	2.9	2.5	4.8	12.8	10.4	0.6	0.9	1.4	0.8	0.1	0.0	0.2	0.1	0.4	0.3	0.4	0.3	3.198		
221509_at	AB014731.1	chromosome 16 BAC clone	7.6	5.4	13.2	48.5	32.4	5.2	5.7	18.1	10.7	3.5	3.8	11.4	2.8	5.6	6.0	4.1	7.5	3.1618		
218637_at	NM_018439.1	CTF9875K-44M2	1.3	2.4	2.9	10.7	9.3	1.5	1.5	2.7	2.1	0.6	0.7	0.6	1.2	0.8	0.7	0.9	1.1	3.1587		
218352_at	NM_018191.1	SMAP-3	0.8	0.5	4.9	13.7	8.7	2.3	1.7	3.4	3.9	1.0	2.0	2.8	0.8	2.3	2.0	1.7	2.2	3.1058		
213035_at	AI081194	hypothetical protein IMPACT	2.1	3.8	11.1	26.7	22.4	2.5	1.5	3.4	2.5	1.9	1.1	2.3	4.6	2.5	1.3	0.1	2.2	3.0937		
211180_x_at	D89788.1	hypothetical protein FLJ0716	1.5	0.2	3.1	9.4	7.5	2.0	2.5	1.7	1.7	1.0	1.4	0.3	0.4	0.4	0.6	1.1	0.7	3.0936		
210731_s_at	AL136105	aml1 (acute myeloid leukemia 1) oncogene	2.1	1.1	4.8	9.1	6.4	1.9	1.8	3.0	1.8	1.2	1.4	2.7	2.1	1.2	1.2	1.7	1.3	3.0876		
203164_at	BE464756	lectin, galactoside-binding, soluble, 8	2.3	1.9	3.7	12.6	12.4	2.5	1.9	4.0	2.7	1.1	0.6	1.2	1.4	2.3	2.6	2.1	2.7	3.063		
205768_s_at	NM_003645.1	(galectin 8)	3.0	1.7	3.9	10.7	7.7	0.4	0.1	0.6	0.2	0.1	0.8	0.7	0.0	0.8	0.1	0.2	0.1	3.0353		
210517_s_at	AB003476.1	acetyl-Coenzyme A transporter	25.1	4.9	44.0	69.5	59.6	1.5	0.4	0.6	0.8	0.1	0.2	1.0	0.9	0.8	0.5	0.1	0.3	3.0146		
210647_x_at	AF102988.1	fatty acid-Coenzyme A ligase, very long-chain 1 (FACVL1)	2.3	1.1	18.7	13.2	9.1	3.4	3.3	4.0	4.5	3.3	5.0	4.2	1.8	3.5	4.4	1.8	2.8	3.002		

Fig. 6B

21/36

B. Eosinophil (Eo)-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pL CD4	CD8	CD14	CD19	Fb	EsL
207328_at	NM_001140.1	15-lipoxygenase	0.1	0.6	0.7	0.1	0.1	14.5	24.6	18.3	17.0	0.1	1.1	0.1	0.1	0.1	0.1	0.0	0.1	0.1	74.129
219695_at	NM_024703.1	FLJ22593	0.0	1.0	1.8	1.8	1.1	29.8	34.7	24.8	27.8	0.8	1.5	0.4	0.9	0.1	0.6	0.4	0.3	0.1	19.123
208253_at	NM_014442.1	sialic acid binding Ig-like lectin, Siglec B	1.3	2.4	0.4	0.4	0.2	17.1	23.1	17.6	11.8	0.1	0.4	0.1	0.8	0.3	0.2	0.1	0.2	0.5	9.8056
211922_s_at	AV028632.1	catalase	3.7	2.2	6.2	6.8	2.2	78.2	134.5	119.7	88.8	16.2	13.0	8.8	8.7	0.7	2.2	2.9	11.1	7.5	9.125
201802_at	NM_004955.1	solute carrier family 29 (nucleoside transporters)	4.8	2.8	2.9	3.4	1.9	24.8	30.4	36.1	42.3	0.1	0.6	0.6	0.8	0.2	0.9	0.3	2.2	1.0	8.989
214523_at	NM_001805.1	CCAAT enhancer binding protein (CEBP), epsilon	0.1	0.1	0.7	1.2	1.2	7.9	11.4	23.4	17.3	1.8	1.5	1.9	1.1	1.4	0.5	0.4	1.0	0.1	8.9462
210029_at	M34455.1	interferon-gamma-inducible indoleamine 2,3-dioxygenase	0.7	0.1	5.3	4.2	2.6	20.0	39.0	33.4	29.5	1.6	2.1	2.3	1.8	1.7	1.5	1.7	0.3	1.4	7.7078
215573_at	AU147084	FLJ12072	0.1	0.1	0.5	0.3	1.1	9.8	8.4	16.9	7.2	0.4	1.9	1.8	2.0	0.1	0.1	0.0	0.1	0.4	7.5983
201801_s_at	AF079117.1	solute carrier family 29 (nucleoside transporters)	3.5	1.9	1.7	0.5	0.9	29.7	47.1	7.4	11.0	0.1	0.5	0.4	0.7	1.1	0.4	0.1	1.4	0.6	7.0314
213825_at	AF221520.1	oligodendrocyte lineage transcription factor 2	0.4	0.6	0.2	0.4	0.6	6.0	10.9	18.7	12.5	0.8	0.9	1.5	1.0	0.6	1.7	0.3	0.4	0.3	6.5987
219821_s_at	NM_018988.1	glucose-fructose oxidoreductase domain containing	3.0	1.4	1.8	2.6	2.3	18.7	17.3	30.9	31.3	3.9	3.1	2.4	2.9	3.2	1.3	2.5	3.0	3.8	6.2284
205472_s_at	NM_004392.1	dachshund (Drosophila) homolog	0.0	0.1	0.1	0.4	0.1	2.7	1.4	2.2	1.7	0.3	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.3	6.0088
202188_at	NM_014669.1	KIAA0095	0.5	0.9	0.4	1.8	1.2	6.8	8.5	13.5	10.6	0.2	0.2	0.2	0.1	0.2	0.3	1.7	1.7	1.4	5.4499
210548_at	U58913.1	chemokine CCL23	0.6	1.8	0.4	1.1	0.5	5.5	6.2	4.2	6.9	0.1	0.9	0.1	0.2	0.3	0.1	0.2	0.6	0.1	5.3082
209447_at	AF043290.1	lymphocyte membrane associated protein (887)	0.6	0.5	2.5	3.4	3.6	41.8	49.7	66.2	60.1	0.2	0.9	0.5	1.2	2.6	5.1	10.4	1.6	6.3	5.1472
206171_at	NM_000677.2	ADORA3 adenosine A3 receptor	2.3	2.8	2.8	3.7	2.2	7.8	13.9	22.0	17.9	1.6	3.1	2.2	2.5	1.2	1.6	0.5	2.0	0.5	5.0469
210549_s_at	U58913.1	chemokine CCL23	1.1	1.1	0.1	1.3	0.6	7.9	5.6	2.7	8.1	0.0	0.6	0.0	0.2	0.1	0.1	0.1	0.2	0.0	4.9873
214183_s_at	X91817.1	transketolase-like protein	0.1	0.2	0.2	0.1	0.1	3.2	4.0	6.6	7.2	0.2	0.2	0.1	0.1	0.2	0.2	1.0	0.1	0.6	4.7894
215350_at	AB033088.1	spectrin repeat containing, nuclear envelope 1	0.1	0.1	0.5	0.1	0.1	3.8	4.2	3.0	2.8	0.0	0.1	0.2	0.4	0.7	0.2	0.1	0.0	0.1	4.7822
206277_at	NM_002564.1	P2Y2 purinergic receptor	0.1	0.1	0.1	0.2	0.1	3.4	4.7	8.1	5.9	0.1	0.3	0.1	0.1	0.2	0.1	0.3	1.2	0.2	4.3043
204776_at	NM_003248.1	thrombospondin 4 (THBS4)	0.8	0.1	1.5	0.1	0.8	3.2	5.9	10.0	6.4	1.8	1.4	0.6	0.9	0.3	0.2	0.3	1.4	1.1	4.1746
201563_at	L29008.1	L-idoitol-2 dehydrogenase	4.1	2.6	3.5	11.4	1.28	22.5	29.9	49.0	37.0	1.8	3.0	4.4	2.2	2.1	1.6	1.2	2.7	2.5	4.1557
206637_at	NM_014879.1	P2YX purinergic receptor GPR105 for UDP-glucose	5.7	1.6	13.3	19.9	1.35	44.2	55.1	81.4	62.4	1.8	9.3	15.4	9.2	0.7	0.9	0.8	0.0	5.5	3.8761
213622_at	A1733465	collagen, type IX, alpha 2	1.5	1.4	1.9	1.2	1.3	10.3	9.6	6.6	8.8	2.7	2.1	2.1	2.2	0.7	1.2	1.2	2.2	1.7	3.8576
214705_at	AJ001306.1	PDZ domain protein	0.1	0.1	0.4	0.3	0.1	2.1	1.5	2.6	2.2	0.3	0.0	0.6	0.7	0.1	0.4	0.3	0.3	0.6	3.6532
266_s_at	L33930	CD24 signal transducer	0.2	0.1	3.0	0.3	0.8	11.9	14.0	18.8	13.9	0.1	0.1	0.3	0.8	0.9	0.0	0.1	0.1	0.1	3.3793
201432_at	NM_001752.1	catalase (CAT)	23.0	14.3	35.7	49.4	1.99	20.3	209.7	221.6	207.3	67.0	54.3	71.3	60.9	9.2	11.2	15.1	53.6	29.9	3.3325
209696_at	D26054.1	fructose-1,6-bisphosphatase	0.9	3.4	4.3	11.1	6.4	20.2	27.7	28.8	32.5	3.0	2.5	2.4	1.5	1.9	2.0	1.6	8.1	1.1	3.3089
216379_x_at	AK000168.1	CD24 signal transducer	1.3	1.4	16.2	0.9	1.5	66.1	70.1	81.9	77.9	1.7	2.8	2.6	4.1	4.8	0.5	0.6	0.9	2.25	3.2741
205569_at	NM_014398.1	lysosome-associated membrane glycoprotein (TSC403)	0.4	0.2	0.7	0.1	0.4	2.4	3.1	6.8	3.0	0.6	0.1	1.4	0.8	0.4	1.1	0.7	0.1	0.0	3.2308
219233_s_at	NM_018530.1	hypothetical protein PRO2521	0.1	1.9	2.1	4.6	5.4	7.5	8.5	21.8	21.2	0.8	0.1	1.5	2.1	0.1	1.1	4.1	0.1	1.4	3.2093
202286_s_at	J04152	gastrointestinal tumor-associated antigen GA733-1	0.9	0.7	1.3	0.3	0.1	1.1	2.5	8.7	1.8	0.4	0.8	0.6	0.6	0.2	0.2	0.7	0.3	0.5	3.1844
206442_at	NM_003007.1	semenogelin I (SEMG1)	0.6	0.1	0.4	0.0	0.1	1.2	3.2	4.9	3.4	0.3	0.2	1.1	1.9	0.1	0.2	0.2	0.9	0.4	3.1837
205733_at	NM_000057.1	Bloom syndrome	1.9	1.1	2.0	2.4	2.2	8.5	6.0	7.5	11.2	2.1	2.0	1.0	1.2	1.2	2.4	1.8	1.1	2.6	3.1427
204392_at	NM_003656.2	calcium/calmodulin-dependent protein kinase I (CAMK1)	4.0	1.1	6.3	8.9	6.4	17.8	19.3	24.9	26.5	0.6	0.2	1.8	1.5	0.1	1.4	1.0	3.0	0.6	3.0763
213497_at	AL050374.1	DKFZp586C1619	1.0	0.7	1.0	1.3	1.6	6.3	6.8	6.8	6.0	2.3	3.0	1.4	2.3	2.0	0.4	0.5	1.6	1.1	3.0099
219296_at	NM_019028.1	similar to ankryin repeat-containing protein AKR1	2.2	1.7	0.2	3.5	1.6	7.3	4.4	8.4	7.4	1.8	2.4	2.4	2.3	0.1	1.4	1.6	1.3	1.9	3.0018

Fig. 6C

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C. Neutrophil (Ne)-selective transcripts (1/7).

Probe set	Accession #	Transcripts	MC	cord blood	MC	Ba1	Ba2	Ba3	Eo1	Eo2	Eo3	Eo4	Ne1	Ne2	Ne3	Ne4	p1	CD4	CD8	CD14	CD19	Fb	NeSL
205403_at	NM_004633.1	Interleukin 1R type II	R	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	127.86
216782_at	AK026679.1	FLJ23026 fs	R	0.0	0.2	0.2	0.1	0.1	0.1	0.1	0.5	0.2	0.2	0.2	0.2	0.2	0.1	0.1	0.1	0.1	0.2	0.2	112.28
210119_at	U73191.1	KCNJ15 inward rectifier potassium channel Kir 1.3	ICN	0.7	1.1	0.1	0.1	0.5	0.1	0.1	0.9	0.6	81.6	98.6	129.0	88.8	0.7	0.2	0.0	0.8	0.0	0.0	107.47
209395_at	M80927.1	chitinase 3-like 1 (cartilage glycoprotein-39)		1.5	0.2	0.9	0.1	0.4	0.3	0.1	8.1	0.1	28.9	25.3	70.7	40.7	0.1	0.0	0.1	0.1	0.1	0.0	79.595
203691_at	NM_002638.1	protease inhibitor 3, skin-derived (SKALP)		0.2	0.1	0.1	0.1	0.8	0.5	0.2	0.4	0.1	16.9	36.7	27.7	24.5	0.1	0.1	0.1	0.1	0.5	0.1	51.901
211372_s_at	U64094.1	Interleukin 1R type II	R	0.1	0.2	0.1	0.1	0.0	0.1	0.5	0.7	0.1	21.6	36.5	31.4	29.9	0.3	0.2	0.0	0.6	0.0	0.0	50.606
207008_at	NM_001557.1	CXCR2 interleukin B receptor, beta	GPR	0.0	0.4	1.1	1.2	1.0	1.3	1.3	2.1	1.2	129.8	168.4	81.5	68.8	2.7	0.3	0.8	0.7	0.6	0.0	39.316
206515_at	NM_008896.1	leukotriene B4 omega hydroxylase (CYP4F3)		0.3	0.1	1.1	0.7	1.2	0.5	0.8	5.9	1.7	56.8	40.3	57.2	48.9	0.2	0.9	0.0	0.7	0.3	0.3	34.919
204007_at	J04162.1	Fc gamma R IIb (CD16)	R	0.8	0.7	1.4	1.5	1.8	1.1	1.8	2.8	1.9	204.5	226.5	194.0	173.3	6.6	1.3	1.3	2.2	2.6	0.1	29.895
204470_at	NM_001511.1	melanoma growth stimulating activity, alpha		1.2	0.0	0.7	0.9	0.1	0.6	0.5	1.2	0.7	19.1	23.0	26.3	48.1	0.1	0.2	0.2	1.0	0.1	0.2	28.189
206025_s_at	AW188198	tumor necrosis factor, alpha-induced protein 6		0.1	0.3	0.1	0.6	0.4	0.6	0.1	0.2	0.1	19.0	29.9	17.2	24.7	0.1	0.2	0.2	0.8	0.3	0.6	26.336
209396_s_at	M80927.1	chitinase 3-like 1 (cartilage glycoprotein-39)		1.8	0.2	1.6	0.4	0.5	0.8	0.5	5.6	0.9	37.9	32.2	52.8	26.7	1.4	0.0	0.0	0.1	0.1	0.4	25.669
211806_s_at	D87291.1	KCNJ15 inward rectifier potassium channel Kir 1.3	ICN	0.9	1.7	2.0	1.4	1.4	2.1	1.3	1.8	1.7	62.2	77.2	77.5	56.8	3.0	1.0	1.1	1.7	0.9	0.7	22.254
221920_s_at	BE677761	mitochondrial solute carrier		0.4	0.8	6.9	0.0	0.2	2.4	1.5	2.2	1.5	59.0	43.2	57.4	46.8	2.5	0.7	0.3	1.8	1.1	1.0	20.163
207094_at	NM_00634.1	CXCR1 interleukin B receptor, alpha	GPR	0.3	0.1	4.2	4.3	4.4	0.3	0.3	0.2	0.3	69.2	81.9	95.3	87.4	0.4	0.3	0.2	0.2	0.1	0.1	19.325
213589_s_at	AW468201	23614 mRNA sequence		0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	5.5	2.7	5.1	4.0	0.1	0.1	0.2	0.1	0.1	0.0	18.973
218963_s_at	NM_015515.1	DKFZP434G032		0.0	0.1	0.5	0.3	0.1	1.1	2.8	2.8	2.0	46.3	32.5	40.3	31.3	0.3	0.3	0.1	0.1	0.1	0.1	18.3
213506_at	BE965369	PAR2 proteinase activated receptor-2	GPR	0.1	0.0	0.0	0.4	0.3	1.2	1.3	4.1	2.3	33.4	35.7	42.4	33.4	0.1	0.7	0.1	1.6	0.4	1.2	18.208
220187_at	NM_024636.1	FLJ23153		0.3	0.1	0.3	0.1	0.1	0.0	0.1	0.5	0.5	16.5	26.3	5.7	7.0	0.0	0.1	0.1	0.7	0.1	0.2	17.111
206026_s_at	NM_007115.1	tumor necrosis factor, alpha-induced protein 6		0.1	0.8	0.4	0.8	0.6	1.1	0.5	0.9	0.1	18.2	23.3	20.0	17.0	0.6	1.0	1.0	1.1	0.1	1.0	17.051
41469_at	L10343	elafin		1.2	0.7	1.2	0.8	0.8	0.9	1.0	0.7	0.8	16.2	39.1	19.5	17.4	1.3	1.4	0.7	0.8	0.5	0.5	15.913
205568_at	NM_020980.2	aquaporin 9	ICN	0.5	0.9	0.1	0.1	0.1	0.3	0.1	1.0	0.1	133.3	136.7	169.0	110.5	0.4	0.9	0.1	8.6	0.1	0.2	15.805
210483_at	BC005043.1	decoy receptor 1, TRAILR3	R	0.1	0.1	0.4	0.9	0.7	1.0	0.9	1.3	1.2	25.8	23.2	9.7	8.6	0.2	0.4	0.3	0.2	0.2	0.1	13.337
215223_s_at	W46388	superoxide dismutase 2		4.4	1.9	1.7	4.9	8.7	5.8	3.3	6.0	8.3	124.6	153.1	142.4	151.8	11.0	1.6	1.1	7.3	2.2	1.5	13.008
210484_s_at	BC005043.1	decoy receptor 1, TRAILR3	R	0.9	0.9	0.9	0.2	0.1	2.2	4.8	0.8	0.6	60.1	86.3	4.7	5.9	0.5	0.6	0.4	0.9	0.4	0.5	12.748
205654_at	NM_000715.4	complement component 4-binding protein, alpha		0.5	1.1	1.3	0.7	0.7	1.5	1.0	1.3	1.4	2.1	20.7	43.6	33.7	1.2	0.3	1.3	1.2	1.2	0.9	12.161
210773_s_at	U81501.1	formyl peptide receptor 2	GPR	0.8	0.1	0.6	0.6	0.3	0.6	0.6	0.6	0.5	86.9	105.0	50.2	59.9	0.1	1.0	0.6	6.0	0.8	0.1	12.14
206222_at	NM_003841.1	decoy receptor 1, TRAILR3	R	1.5	0.8	1.9	0.7	0.7	3.6	13.7	3.4	3.9	121.0	137.1	37.5	22.5	0.0	0.1	0.1	1.8	0.5	0.7	12.034
207083_s_at	NM_003003.1	SEC14 (S. cerevisiae)-like 1		0.8	0.2	0.9	1.8	3.0	2.2	2.6	3.8	2.6	36.7	25.9	33.9	32.6	1.3	0.1	0.1	1.1	1.0	0.7	11.729
211163_s_at	AF012536.1	decoy receptor 1, TRAILR3	R	0.2	0.1	2.2	1.5	0.6	2.6	12.3	9.4	6.4	87.9	110.9	60.4	55.8	0.5	0.2	0.1	0.7	0.1	0.6	11.404
205931_s_at	NM_004904.1	CAMP response element-binding protein CRE-BPa		0.0	0.1	0.3	0.1	0.6	0.6	0.6	0.6	0.7	23.2	14.5	20.5	12.9	1.6	0.8	0.1	1.6	0.1	0.1	10.618
205922_at	NM_004665.1	vanin 2		0.1	0.0	1.2	2.6	3.9	1.0	0.2	1.9	0.3	114.5	114.6	174.1	189.2	0.1	1.4	4.0	13.8	1.7	0.0	10.451
210176_at	AL050262.1	Toll-like receptor 1	R	0.7	0.6	0.2	0.3	0.3	0.5	1.1	1.9	1.2	29.5	38.6	25.1	32.6	1.6	0.8	0.7	3.0	1.5	0.3	10.418
215977_x_at	X68285.1	glycerol kinase		1.9	0.9	0.8	0.7	1.0	0.3	0.6	0.9	1.0	15.8	19.8	9.7	10.9	0.1	0.1	0.2	0.2	0.2	0.3	10.203
215783_s_at	X14174.1	liver-type alkaline phosphatase		0.5	1.2	0.7	0.9	0.4	0.7	0.5	1.0	0.6	21.2	42.8	11.6	12.8	1.2	0.7	0.2	0.5	0.5	1.9	10.167
217167_x_at	AJ525550	GK gene for glycerol kinase, exon 1		1.2	0.1	0.2	0.3	1.0	0.2	0.1	0.8	0.3	8.0	13.6	7.5	7.2	0.4	0.1	0.1	0.9	0.2	0.2	10.067
213349_at	A934439	KIAA0779		0.9	0.7	0.9	1.4	1.0	1.9	1.4	2.3	2.1	15.6	15.3	19.5	23.8	0.1	1.4	1.5	1.6	1.2	1.2	9.7704

Fig. 6D

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C. Neutrophil (Ne)-selective transcripts (2/7).

Probe set	Accession #	Transcripts	MC	cord blood	MC	Ba1	Ba2	Ba3	Eo	Eo	Eo3	Eo4	Ne	Ne	Ne3	Ne4	p1	CD4	CD8	CD14	CD19	Fb	Ne.S1
210789_x_at	U05921	carcinoembryonic antigen (CEM1)	1.1	0.4	1.9	1.4	1.5	2.0	1.5	2.5	2.5	0.4	194	186	226	155	0.7	1.6	0.9	2.0	0.3	1.1	92749
210772_at	M88107.1	formyl peptide receptor 2	0.1	0.2	0.4	0.7	0.7	0.7	0.3	0.8	0.8	0.7	514	67.7	448	464	0.5	0.5	0.5	5.6	0.1	0.1	92661
218978_s_at	NM_018596.1	PRO1584	0.7	0.5	1.6	0.2	0.5	1.1	0.9	0.7	0.7	0.5	263	20.5	66	2.8	0.2	0.7	0.4	1.1	0.2	0.4	91536
204006_s_at	NM_000570.1	R	0.7	0.2	1.2	0.7	0.6	0.7	0.8	0.0	0.0	0.7	230.7	278.8	47.6	45.9	4.2	1.9	6.9	12.0	3.9	0.1	90769
207275_s_at	NM_001995.1	Fc gamma R IIb (CD16)	4.3	2.6	5.1	11.5	194	53	5.1	5.9	5.9	3.7	93.8	127.8	92.8	69.1	0.7	1.0	1.1	8.3	0.9	1.7	89855
220302_at	NM_005906.2	fatty acid-Coenzyme A ligase, long-chain 1 (FACL1)	0.1	0.0	1.3	0.7	0.8	0.7	0.2	2.0	2.0	1.4	7.9	8.4	7.9	8.9	0.3	0.1	0.0	0.1	0.1	0.0	8866
221803_s_at	AA883074	male germ cell-associated kinase nuclear receptor binding factor-2	1.1	0.8	3.2	4.0	2.9	2.8	2.8	4.7	4.7	3.2	24.7	25.2	33.2	29.3	0.1	1.5	1.2	1.7	2.0	2.6	83788
206765_at	AF153820.1	KCNJ2 inwardly-rectifying potassium channel Kir2.1	1.0	0.4	2.5	4.4	4.4	2.4	4.7	6.1	6.1	8.0	25.8	36.2	52.4	48.3	0.4	0.2	0.5	1.5	0.7	1.1	8108
213351_s_at	AI934469	KIAA0779	0.0	0.1	0.9	2.0	1.6	0.8	0.6	2.3	2.3	2.7	7.9	5.9	20.1	18.0	0.2	0.5	0.2	0.1	0.2	1.2	79705
214590_s_at	AL545760	ubiquitin-conjugating enzyme E2D1 leukotriene B4 omega hydroxylase (CYP4F3)	0.1	1.5	0.3	0.4	0.5	1.1	1.0	0.5	0.5	0.4	7.9	10.7	10.1	4.4	0.1	0.4	0.3	1.0	0.4	0.9	78712
206522_at	NM_004668.1	R	0.0	0.0	0.8	1.8	1.0	3.0	5.4	11.7	11.7	9.4	46.0	51.5	56.9	43.0	0.1	0.0	0.0	0.6	0.6	0.1	75773
210992_x_at	U90939.1	Fc gamma receptor IIC2	1.9	1.0	1.7	2.1	3.3	8.1	16.1	2.8	2.8	4.2	70.9	95.6	42.8	30.5	0.3	0.2	0.1	7.2	2.3	0.2	75239
220528_at	NM_018399.1	VAN3 protein	0.1	0.2	1.3	6.1	5.0	0.2	0.1	0.5	0.5	0.4	26.8	22.1	20.0	36.8	0.8	0.2	0.1	3.0	0.1	0.1	75216
200919_at	NM_004427.1	early development regulator 2	5.6	4.4	4.8	6.5	9.6	7.6	6.8	5.3	5.3	7.3	109.5	89.0	52.9	61.4	2.5	4.9	7.0	10.0	3.9	6.5	75056
207387_s_at	NM_000167.1	glycerol kinase	2.1	1.5	1.0	1.5	1.6	1.1	1.4	1.6	1.6	1.4	14.3	20.3	10.7	10.3	0.9	0.6	0.3	1.7	0.6	0.6	74603
117_at	X51757	heat-shock protein HSP70B	1.1	0.2	0.8	0.6	0.9	5.9	8.3	2.1	2.1	4.1	46.3	41.2	25.1	25.8	0.4	0.9	0.6	3.7	1.6	0.5	74139
205174_s_at	NM_012413.2	glutaminyl-peptide cyclotransferas triggering receptor expressed on myeloid cells 1	0.4	0.0	0.4	0.7	0.9	0.7	0.0	0.4	0.4	0.3	30.1	47.7	36.4	24.7	0.7	0.6	0.0	4.6	0.1	1.5	73246
219434_at	NM_018643.1	thrombomodulin	1.3	0.3	0.4	0.2	0.5	2.9	0.7	1.4	1.4	1.5	92.8	84.0	81.2	98.6	3.4	0.6	0.1	12.3	0.9	0.3	72388
203887_s_at	NM_000361.1	orosomucoid 1 (ORM1)	1.7	0.1	0.4	0.4	0.4	0.2	1.0	1.4	1.4	1.1	16.8	13.0	13.4	1.3	0.7	0.6	0.4	1.1	0.4	0.2	71328
205040_at	NM_000607.1	glycerol kinase	0.5	0.1	0.1	0.4	0.1	0.1	0.0	1.1	1.1	0.0	3.4	4.1	4.3	0.7	0.1	0.3	0.1	0.4	0.0	0.2	70823
214681_at	AI830490	glycerol kinase	0.2	0.4	0.1	1.2	1.7	0.8	1.1	0.6	0.6	1.2	7.8	14.2	24.0	12.1	0.9	0.0	0.1	1.9	1.0	0.3	6966
218035_s_at	NM_019027.1	FLJ20273	2.9	1.0	0.9	1.5	0.8	0.9	0.4	1.3	1.3	1.1	47.2	54.4	91.9	94.0	1.7	0.7	0.4	9.9	1.5	0.3	69074
205068_s_at	BE671084	GTPase regulator associated with the focal adhesion kinase pp125(FAK)	1.2	1.4	3.5	5.9	5.1	6.5	5.1	8.5	8.5	7.1	43.7	40.6	45.2	56.0	0.7	1.3	2.9	5.1	0.8	1.2	68934
203021_at	NM_003064.1	secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI)	1.7	0.8	4.6	1.5	1.1	1.2	2.2	8.5	8.5	0.8	16.2	19.8	13.9	8.7	1.8	0.6	1.2	1.7	1.1	2.1	67497
216316_x_at	X78713	glycerol kinase pseudogene, chromosome 1	2.0	0.9	0.4	0.6	1.0	0.7	0.6	0.5	0.5	1.0	10.3	18.6	5.8	5.8	0.5	0.2	0.2	0.8	0.3	0.1	66675
217209_at	X16454	carcinoembryonic antigen subdomains A and B	0.6	0.4	0.2	0.2	0.4	0.1	0.3	0.7	0.7	0.5	2.8	3.8	3.3	2.7	0.3	0.4	0.0	0.1	0.1	0.2	65382
220421_at	NM_024850.1	FLJ21458	0.3	0.6	0.1	0.1	0.1	0.3	0.8	0.4	0.4	0.3	8.9	7.2	9.1	7.0	1.2	0.6	0.0	0.1	0.1	0.2	64857
213524_s_at	NM_015714.1	putative lymphocyte G0G1 switch gene (G0S2)	0.8	0.8	1.3	0.9	0.5	8.0	8.5	18.7	18.7	10.1	118.0	52.0	39.6	92.5	1.7	0.8	0.1	6.0	0.2	3.4	64779
206472_s_at	NM_005078.1	transducin-like enhancer of split 3	2.2	2.6	1.3	0.7	0.5	1.6	0.6	0.5	0.5	1.0	22.6	25.0	11.3	8.3	1.3	1.2	1.5	1.8	1.5	0.9	64334
212769_at	AI567426	KIAA1547	1.4	1.5	0.5	1.3	2.3	1.1	1.0	2.2	2.2	1.9	17.9	15.9	15.1	12.8	2.4	0.8	1.1	1.3	1.2	0.5	64271
204307_at	AB002295.1	KIAA0329	0.7	0.0	0.1	2.6	2.1	1.8	1.5	2.4	2.4	2.0	10.3	11.2	15.4	12.8	1.9	0.1	0.5	0.2	0.1	0.5	63478
203591_s_at	NM_000760.1	R	0.1	0.0	1.0	0.1	0.2	2.3	0.6	2.4	2.4	1.0	220.3	187.2	134.9	112.1	0.2	0.8	0.2	25.5	0.1	0.2	62051
210210_at	AF181660.1	granulocyte colony-stimulating factor receptor	0.9	1.1	1.6	1.8	1.9	1.1	1.9	1.7	1.7	2.0	11.1	7.0	13.7	14.1	1.4	1.3	0.9	1.6	1.1	0.6	6172
218610_s_at	NM_018340.1	immunoglobulin superfamily member WM78	1.5	1.2	1.2	1.2	1.8	3.3	3.2	2.6	2.6	1.8	25.2	23.3	17.9	21.8	0.5	0.6	0.4	3.6	0.4	0.6	6112
203561_at	NM_021642.1	R	4.7	1.2	0.9	1.2	2.4	19.5	22.8	19.4	19.4	21.4	104.3	129.0	153.0	123.9	4.0	0.7	0.7	16.3	2.2	0.2	61015
216841_s_at	X15132.1	Fc gamma receptor Ila (CD32) superoxide dismutase 2	1.3	1.1	1.2	1.8	2.2	1.4	1.3	3.2	3.2	2.4	20.5	44.6	35.8	42.2	5.6	0.8	0.7	2.0	0.7	1.1	60724

Fig. 6E

C. Neutrophil (Ne)-selective transcripts (3/7).

Probe set	Accession #	Transcripts	MC cond blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl CD4	CD8	CD14	CD19	Fb	NeSL
207624_s_at	NM_000328.1	retinitis pigmentosa GTPase	0.0	0.6	1.1	2.0	1.2	1.1	1.2	2.1	2.8	7.1	7.0	13.6	15.1	0.2	1.2	0.9	0.7	0.3	60348
209850_s_at	BC005406.1	regulator (RPR)	0.2	0.2	1.3	0.2	1.0	0.2	0.4	0.5	0.4	13.2	9.6	6.7	8.7	0.2	0.2	0.6	0.4	1.6	59313
203936_s_at	NM_004994.1	Cdc42 effector protein 2	47.7	0.6	1.6	1.9	1.4	1.2	2.4	15.5	1.5	36.5	35.1	36.8	21.9	1.7	2.0	1.4	1.3	1.4	59311
215966_x_at	AA292874	matrix metalloproteinase 9 glycerol kinase	1.2	0.2	0.6	0.1	1.2	0.2	1.0	1.2	1.2	6.6	10.2	7.3	7.4	0.2	0.1	0.2	0.5	0.0	59077
206925_at	NM_005668.1	sialyltransferase 8	3.1	1.2	2.1	2.5	2.0	1.4	3.1	1.6	1.6	21.7	33.3	6.8	11.4	0.4	0.9	1.6	1.2	0.2	58688
211764_s_at	BC005980.1	ubiquitin-conjugating enzyme E2D 1 (PITPN)	1.8	1.4	1.1	2.9	2.4	7.5	5.7	3.9	2.2	29.3	31.2	52.6	25.4	0.2	2.0	1.4	1.3	2.3	58143
201192_s_at	NM_006224.1	phosphatidylinositol transfer protein	3.0	3.1	1.9	5.0	4.6	3.9	5.4	6.6	5.4	27.9	26.9	32.9	35.2	2.0	3.5	3.7	3.2	2.8	5811
205921_s_at	U16120.1	placental taurine transporter	1.2	0.7	0.5	0.2	0.4	0.3	1.6	0.5	0.9	14.8	17.2	2.8	2.6	0.0	0.1	0.3	0.3	0.4	57909
209137_s_at	BC000263.1	ubiquitin C-terminal hydrolase related polypeptide	3.6	4.1	2.0	2.6	1.9	1.5	0.9	2.7	0.9	25.0	24.5	37.6	29.7	3.5	5.0	2.5	2.7	3.0	57864
208052_x_at	NM_001815.1	carcinoembryonic antigen-related cell	1.7	1.4	2.9	2.7	1.9	3.0	2.6	2.8	2.1	14.3	16.5	20.0	13.7	2.5	1.3	2.3	2.5	1.6	57572
201393_s_at	NM_000876.1	adhesion molecule 3 (CEACAM3)	6.4	2.8	0.2	0.8	1.8	4.1	5.4	6.8	5.4	82.4	106.9	80.1	71.7	1.7	2.9	8.7	4.8	14.8	57104
218614_at	NM_018169.1	insulin-like growth factor 2 receptor	1.2	1.0	6.9	13.7	12.5	3.2	3.3	7.7	5.8	52.7	54.4	82.8	83.3	2.9	8.7	11.8	10.8	1.3	56442
202084_s_at	NM_003003.1	FLJ10652	5.7	2.5	12.8	28.8	22.6	20.6	18.7	35.5	29.5	130.7	129.7	135.6	177.9	19.2	4.1	3.5	11.5	7.7	56423
32069_at	AB014515	SEC14 (S. cerevisiae)-like 1 KIAA0615	2.8	1.5	2.1	5.6	5.5	4.6	3.7	5.9	6.9	23.9	20.9	35.1	40.5	1.0	3.4	3.3	2.6	2.1	56348
205896_at	NM_003059.1	solute carrier family 22 member 4 (SLC22A4)	0.8	1.2	1.0	0.1	1.1	1.9	2.4	3.5	2.7	8.5	13.3	30.0	12.6	0.5	0.7	0.8	0.5	1.4	54612
206584_at	NM_015364.1	MD-2 protein	7.4	1.1	2.0	3.9	1.8	1.0	0.4	0.6	0.5	43.9	62.3	87.8	56.0	1.3	3.5	1.0	11.1	3.5	54459
202082_s_at	NM_003003.1	SEC14 (S. cerevisiae)-like 1	1.0	0.3	3.6	2.5	2.2	15.5	5.4	12.3	8.4	40.2	57.3	54.9	60.9	3.8	0.8	1.3	2.7	3.3	54422
204308_s_at	NM_014844.1	KIAA0329	2.9	1.1	2.2	2.8	2.8	2.1	3.1	3.1	4.3	16.5	18.7	19.9	19.0	3.4	1.3	1.7	1.8	1.3	54369
207500_at	NM_004347.1	caspase 5	0.3	1.1	0.1	0.0	0.1	0.1	0.3	0.2	0.5	4.2	6.2	4.6	2.9	0.3	0.3	0.4	0.8	0.1	5379
203435_s_at	NM_007287.7	CD10, membrane metallo-endopeptidase	0.3	0.5	0.4	0.3	0.2	0.1	0.3	0.3	0.2	16.4	44.2	54.6	42.8	0.2	0.3	0.2	0.2	0.2	52591
205539_at	NM_006576.1	advinin	0.4	0.5	2.0	1.4	0.8	1.0	1.1	1.0	1.1	8.4	6.9	6.0	10.1	1.0	1.3	0.4	1.5	0.7	52541
204601_at	NM_014664.1	KIAA0615	1.9	1.2	1.3	3.2	2.3	3.0	2.7	3.7	3.0	12.9	12.8	20.2	20.0	0.1	2.2	2.6	1.3	1.9	52381
201963_at	NM_021122.2	fatty acid-Coenzyme A ligase long-chain 1 (FACL1)	2.9	2.1	5.0	19.9	33.4	6.6	3.8	10.3	6.1	58.8	86.6	92.2	80.2	0.1	1.1	1.1	10.8	1.5	52374
207064_s_at	NM_009590.1	CXCR1 Interleukin 8 receptor, alpha	0.7	0.1	0.9	0.9	0.8	0.8	0.8	0.9	1.2	4.3	4.7	4.0	6.6	0.8	0.5	0.8	0.5	0.8	51905
220005_at	NM_023914.1	P2YX purinergic receptor GPR86 for UDP-glucose	0.6	0.0	0.1	0.5	0.1	19.7	9.6	25.1	17.3	76.5	77.1	100.7	98.6	1.9	0.1	0.2	12.3	0.6	51686
211395_x_at	U90940.1	Fc gamma receptor IIC3	4.6	0.3	7.3	9.7	15.1	9.7	19.5	4.4	6.6	115.0	140.3	42.9	38.9	3.0	1.4	0.6	14.0	7.2	51401
201780_s_at	NM_007282.1	ring finger protein 13 (RNF13)	4.4	2.8	3.5	9.2	6.6	6.8	6.2	8.9	7.1	27.1	36.6	52.5	35.7	0.8	4.1	3.7	7.2	4.6	51305
209864_at	AB045118.1	GSK-3 binding protein FRAT2	2.8	1.3	4.4	9.2	8.0	13.4	16.9	27.3	22.6	93.2	97.2	100.6	104.2	1.3	1.9	2.9	10.2	2.5	51047
218319_at	NM_020651.2	pellino (Drosophila) homolog 1 (PELL1)	3.4	2.9	5.9	17.5	33.5	17.7	11.7	12.6	15.1	64.9	88.3	73.0	80.2	2.4	6.3	2.9	13.8	1.1	50403
206632_s_at	NM_004900.1	phorbollin	0.6	1.1	1.0	1.2	2.6	1.3	0.8	3.9	0.5	19.6	11.1	30.8	0.5	1.5	0.2	0.4	0.4	1.0	50277
220990_s_at	NM_030938.1	DKFZp5661133	11.7	6.2	4.6	18.5	12.5	5.0	3.3	8.2	4.9	115.5	117.2	125.3	122.5	2.6	5.3	4.2	24.1	4.4	49858
221653_x_at	BC004395.1	apolipoprotein L	0.7	2.8	0.6	2.1	1.6	2.0	0.4	1.8	1.1	8.0	3.9	12.7	5.2	0.2	0.9	0.4	1.4	1.1	49332
204748_at	NM_00963.1	COX2 prostaglandin-endoperoxide synthase 2	6.5	16.2	0.6	2.4	2.0	4.5	2.3	3.4	3.4	35.8	44.1	44.6	91.8	0.4	0.6	0.2	4.3	0.3	49206
210423_s_at	L32185.1	integral membrane protein	2.0	0.2	1.4	1.6	1.3	1.3	2.2	1.5	2.0	85.0	78.5	75.2	52.9	1.9	0.4	1.9	14.7	1.0	48845
206429_at	NM_005242.2	PAR2 proteinase activated receptor-2	0.8	0.8	0.9	0.2	0.9	0.9	1.1	0.2	0.8	11.8	15.1	4.1	4.1	1.3	1.5	0.2	1.5	0.3	48608
213352_at	A1934469	KIAA0779	0.6	0.9	1.2	1.5	1.2	1.2	1.5	1.5	2.2	8.4	6.0	8.7	7.7	1.6	0.9	1.5	1.0	1.3	48373
201888_s_at	U81379.3	interleukin-13 receptor	0.1	0.6	0.3	0.2	0.0	1.7	2.7	1.7	2.0	8.6	19.0	15.0	13.9	0.4	0.4	0.3	2.9	1.3	4746

Fig. 6F

C. Neutrophil (Ne)-selective transcripts (4/7).

Probe set	Accession #	R	Transcripts	MC	MC	Ba1	Ba2	Ba3	EO	EO	EO4	Ne	Ne	Ne3	Ne4	CD4	CD8	CD14	CD19	Fb	Ba.SL	
204780_s_at	AA164751		CD95, Fas, APO-1	1.4	1.4	7.2	14.0	11.5	6.6	6.7	6.5	4.53	38.8	65.5	51.8	1.3	5.6	4.8	3.6	2.6	9.7	4.7254
209310_s_at	U25804.1		Ich-2 cysteine protease phosphatidylinositol glycan, class B (PIGB)	2.5	1.9	2.1	7.7	7.0	1.4	1.3	1.4	19.1	17.5	36.7	23.5	2.9	4.1	4.5	4.9	3.9	2.2	4.6817
205452_at	NM_004855.1		FLJ20950	2.3	2.7	2.3	6.4	7.7	2.3	1.4	3.0	16.3	17.6	22.2	39.3	1.7	2.0	2.9	2.8	3.5	2.2	4.6577
218298_s_at	NM_024952.1		swine acylneuraminase lyase	3.1	3.3	5.4	8.1	7.2	5.7	5.7	9.4	37.2	23.4	37.3	39.1	0.6	1.7	3.1	5.8	2.3	2.7	4.6558
221210_s_at	NM_030769.1		chromosome 1 open reading frame	3.8	1.2	0.8	1.2	1.4	3.0	4.7	4.6	20.4	23.6	23.5	18.3	0.6	0.1	0.3	4.6	0.5	0.1	4.6378
221497_x_at	BC005369.1		12, clone MGC12484	3.0	2.4	4.3	5.7	5.9	3.3	7.6	5.4	29.3	32.4	24.3	21.5	1.8	3.1	2.9	2.9	1.9	2.0	4.6333
204668_at	AL031670		ferritin, light polypeptide-like 1	0.8	0.5	1.8	1.0	1.2	0.3	1.5	0.9	8.4	8.1	7.0	6.5	1.4	1.3	1.0	1.5	0.5	1.6	4.614
201921_at	NM_004125.1		guanine nucleotide binding protein 10 (GNNG10)	7.1	5.4	2.6	6.7	6.5	11.7	11.4	15.3	45.5	87.5	81.3	57.1	0.8	2.7	3.0	8.4	3.2	12.4	4.5644
209600_s_at	S69189.1		peroxisomal acyl-coenzyme A oxidase	2.9	1.7	2.8	5.3	4.7	1.4	1.0	1.3	15.0	17.7	21.4	21.2	0.4	1.0	0.8	2.1	0.7	1.5	4.5552
205119_s_at	NM_002029.1		formyl peptide receptor 1	4.1	1.4	11.2	26.6	32.7	14.0	11.1	6.0	288.2	315.8	274.7	252.9	3.6	1.3	0.7	62.6	1.1	0.5	4.505
217738_at	BF575514		pre-B-cell colony-enhancing factor	5.7	0.9	7.4	24.1	34.9	7.5	4.6	3.9	73.4	87.0	89.9	79.9	2.2	1.7	1.6	10.1	1.7	2.8	4.4839
215078_at	AL050388.1		DKFZp564M2422	0.0	0.1	0.0	0.1	0.4	0.9	0.5	0.3	7.1	12.9	4.5	7.9	0.1	0.5	0.5	1.7	0.1	0.1	4.4343
207545_s_at	NM_003744.1		numb (Drosophila) homolog	0.7	1.4	1.1	2.5	2.4	2.7	1.8	1.2	7.2	11.2	10.5	7.4	0.8	0.5	0.5	1.6	1.1	1.2	4.3728
213418_at	NM_002155.1		heat shock 70kD protein 6 (HSP70B)	1.1	0.4	0.7	1.5	1.6	2.5	2.8	17.0	104.0	91.6	70.0	70.8	0.5	1.1	1.1	12.8	4.7	0.5	4.3655
218023_s_at	NM_016605.1		putative nuclear protein (LOC51307)	5.7	3.8	6.6	13.0	12.6	8.5	10.3	10.9	40.1	39.7	47.0	59.7	3.0	4.4	5.9	7.0	6.0	6.8	4.3383
210386_s_at	BC001906.1		Similar to metaxin 1	6.2	1.9	2.7	5.4	4.0	1.4	2.2	3.6	19.5	15.8	23.4	23.8	2.5	3.6	2.6	4.1	2.6	4.7	4.3318
207643_s_at	NM_001065.1		CD120a, TNF-R1 p55	1.8	1.6	0.9	1.3	1.4	6.3	7.4	9.0	81.1	83.6	68.6	65.6	1.3	2.2	5.9	17.4	0.6	16.0	4.2796
203140_at	NM_001706.1		B-cell CLL lymphoma 6 (BCL6)	6.2	2.9	9.1	13.5	19.8	23.5	16.7	33.1	99.1	107.8	115.8	101.1	2.2	3.4	3.4	23.4	6.7	6.5	4.2767
207253_s_at	NM_016936.1		ubiquitin 1	3.2	2.8	2.9	4.4	5.0	3.8	2.6	3.6	16.7	20.0	14.2	17.8	2.3	2.5	2.5	2.2	2.4	1.8	4.2556
202875_s_at	BE397715		pre-B-cell leukemia transcription factor 2	2.0	1.4	0.1	0.1	0.2	2.5	3.6	1.5	11.6	15.4	6.8	7.5	0.8	1.7	1.9	1.1	1.3	0.7	4.2425
218791_s_at	NM_024713.1		FLJ22557	1.2	0.7	2.5	2.7	1.8	0.9	1.5	1.0	6.9	8.7	13.2	11.2	1.4	1.0	0.5	1.3	0.8	1.2	4.2114
211862_x_at	AF015451.1		Usurpin-beta bromodomain adjacent to zinc finger domain, 1A	3.5	2.6	16.8	9.7	10.1	5.6	10.2	7.1	65.7	67.7	36.1	37.9	3.1	6.8	8.7	10.1	6.9	2.0	4.2001
217986_s_at	NM_013448.1		niban	3.5	3.0	3.5	9.2	8.4	6.1	8.5	13.1	39.0	35.1	43.5	51.6	2.5	5.9	6.5	7.0	5.0	1.7	4.1976
217966_s_at	NM_022083.1		KIAA0993	4.1	1.9	6.4	7.4	9.0	24.2	14.8	11.8	51.9	105.3	76.2	80.0	0.9	3.3	3.8	3.2	2.0	8.2	4.1858
212602_at	A1806395		CASP8 and FADD-like apoptosis regulator (FLAR)	2.3	3.5	0.4	0.9	1.1	0.8	0.6	0.8	17.1	18.1	12.9	13.4	1.5	0.5	0.3	3.6	0.8	2.8	4.1806
208485_x_at	NM_003879.1		gp 180-carboxypeptidase D-like enzyme	3.2	2.5	19.2	9.8	9.9	6.2	13.0	8.1	70.8	69.7	33.8	41.4	3.5	6.4	8.4	11.5	6.6	2.0	4.1719
201942_s_at	D85390.1		FLJ13409	0.6	1.7	0.6	1.3	1.7	1.6	7.0	2.6	15.9	23.8	6.8	8.1	0.5	0.8	1.3	2.5	0.5	2.6	4.1525
220933_s_at	NM_024617.1		glycerol-3-phosphate dehydrogenase	2.1	2.0	9.6	14.2	14.0	7.1	7.2	12.5	38.1	37.3	81.5	57.8	1.9	3.1	4.8	6.2	3.8	3.0	4.1025
221764_at	AL574186		Toll-like receptor 6	6.3	4.4	16.5	18.6	15.0	10.4	15.8	22.7	80.9	99.2	46.3	60.3	9.5	8.9	9.4	5.7	9.4	2.5	4.0745
207446_at	NM_006068.1		chromosome 6 open reading frame 76	0.5	0.5	0.7	1.5	0.8	0.8	0.9	0.8	7.6	11.8	7.2	8.7	0.1	0.9	0.9	2.1	1.2	0.6	4.0697
219748_at	NM_024807.1			0.2	0.3	0.3	0.4	0.6	1.9	2.6	1.6	9.1	9.1	6.7	6.4	0.2	0.3	0.6	0.5	1.1	0.0	4.0619
220945_x_at	NM_018050.1		FLJ10298	1.0	1.4	0.5	0.7	0.7	1.1	0.6	1.0	8.0	10.8	13.6	11.0	1.1	0.5	0.3	0.9	0.6	2.6	4.057
212577_at	AA888754		KIAA0650	1.9	1.3	6.4	8.0	9.9	10.1	24.0	9.4	74.0	98.6	42.2	57.4	4.4	10.8	9.5	7.5	16.0	3.2	4.0417
221732_at	AK026161.1		RIKEN cDNA 5830420C20	2.8	0.7	3.4	10.5	8.8	5.0	6.0	10.9	27.6	31.6	30.8	34.7	0.3	0.4	1.8	2.5	1.6	4.6	4.041
205986_at	NM_004920.1		apoptosis-associated tyrosine kinase	1.6	1.3	0.7	1.0	0.5	0.3	0.3	1.4	10.5	15.8	13.3	15.2	3.2	1.0	0.5	3.4	0.9	0.4	4.0322
213501_at	T62985		acyl-Coenzyme A oxidase 1, palmitoyl	1.3	1.1	2.0	2.6	2.8	1.3	0.9	0.6	8.5	11.5	12.4	7.5	0.1	1.1	0.3	1.8	0.5	1.1	4.0194
204542_at	NM_006456.1		sialyltransferase (ST6M)	0.4	0.2	1.5	0.3	0.2	3.4	3.9	3.2	13.0	13.4	21.0	13.4	0.7	0.7	0.3	1.4	0.3	0.6	4.016

Fig. 6G

C. Neutrophil (Ne)-selective transcripts (5/7).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	EO 1	EO 2	EO3 (small)	EO4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	CD4	CD8	CD14	CD19	Fb	NeSL
204071_s_at	NM_005802.1	tumor protein p53-binding protein	1.4	1.6	1.1	3.0	2.9	3.7	2.3	2.6	2.2	10.5	12.8	8.0	11.9	2.2	2.2	1.4	2.2	2.1	4.0148
210594_x_at	AF239756.1	myelin protein zero-like 1	1.2	0.5	0.6	1.5	1.2	0.1	0.4	0.8	1.9	15.3	13.9	7.1	10.9	0.3	0.2	1.0	0.7	2.8	3.9778
203063_at	NM_014634.1	protein phosphatase 1F (pp2C domain containing)	0.5	0.4	1.4	3.3	3.0	4.0	6.0	6.1	10.0	33.1	22.2	29.6	31.8	0.3	2.9	1.2	7.3	1.5	3.9764
201392_s_at	BG031974	insulin-like growth factor 2 receptor	1.7	0.7	0.1	0.0	0.1	2.6	3.0	1.9	1.5	51.1	59.1	12.8	15.0	1.1	1.2	4.0	3.8	2.2	3.9602
221477_s_at	BF575213	MGC5618	2.9	1.4	3.4	4.3	9.0	4.2	4.2	4.2	4.2	56.8	63.6	36.1	46.6	7.9	3.2	1.2	2.7	2.1	3.9562
206756_at	NM_019886.1	carbohydrate (N-acetylglucosamine 6-O)sulfotransferase 7	0.2	0.1	0.1	0.0	0.1	0.1	0.1	0.1	0.1	5.0	3.9	3.5	10.5	0.1	1.3	1.0	0.2	0.5	3.9516
204994_at	NM_002463.1	myxovirus (influenza) resistance 2 (MX2)	1.3	2.3	5.4	7.8	8.2	9.2	11.6	15.2	12.3	49.8	46.6	77.6	80.8	2.4	7.5	6.0	4.8	1.8	3.9478
201943_s_at	NM_001304.2	carboxypeptidase D	0.9	0.9	0.5	2.1	3.6	1.7	7.6	7.2	4.6	16.4	21.3	18.7	15.2	0.7	1.0	1.7	3.3	0.4	3.8926
216252_x_at	Z70519.1	CD95, Fas, APO-1	0.3	0.8	4.3	2.5	1.1	1.8	4.7	1.8	1.7	18.5	31.2	10.3	8.4	2.2	3.8	2.4	1.9	1.4	3.8691
203066_at	NM_014863.1	B cell RAG associated protein (BRAG)	1.3	3.9	0.9	1.2	1.0	10.6	10.2	13.1	20.2	57.0	65.9	95.2	86.9	1.9	0.1	0.0	4.2	5.9	3.8667
212479_s_at	AL050139.1	FLJ13910	1.7	1.6	2.1	2.5	2.6	2.4	2.5	3.5	1.7	9.0	10.1	8.8	9.8	1.1	2.3	2.4	2.2	1.9	3.8422
209571_at	U03644.1	receptin	0.7	0.2	1.6	3.3	2.7	2.2	1.3	2.6	2.7	6.8	7.8	12.8	10.9	0.8	1.0	1.1	1.2	1.5	3.8367
211317_s_at	AF041461.1	CASP8 and FADD-like apoptosis regulator	1.6	1.8	9.5	3.6	4.0	3.7	6.8	3.2	2.8	33.1	44.8	15.2	17.6	2.4	4.7	6.5	5.7	4.9	3.8332
209732_at	BC005254.1	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2	8.1	5.9	10.0	18.6	23.6	9.0	10.0	8.9	7.3	72.9	77.0	99.7	75.5	4.1	14.4	21.2	10.2	16.4	3.8003
201779_s_at	AF070558.1	clone 24450 RING zinc finger protein RZF	1.48	5.9	13.0	13.3	13.9	21.8	27.0	25.3	13.1	88.2	108.1	116.5	81.8	6.0	9.6	11.3	25.7	15.7	3.7993
212441_at	D86985.2	KIAA0232	5.4	2.9	3.5	9.8	10.3	8.0	6.9	11.5	11.3	31.9	30.1	30.8	49.8	2.5	2.0	4.0	5.9	2.1	3.7868
205920_at	NM_003043.1	solute carrier family 6, member 6 (SLC6A6)	1.2	1.4	0.9	0.2	0.2	1.1	5.2	0.7	1.4	33.1	26.7	2.7	4.0	0.3	0.1	0.4	2.6	0.1	3.7836
213596_at	AL050391.1	DKFZp586A181	0.7	0.7	2.3	3.6	3.0	1.2	1.2	1.1	1.2	10.6	10.9	12.5	9.9	2.2	1.1	2.0	1.5	0.7	3.7615
209508_x_at	AF005774.1	caspase-like apoptosis regulatory protein (clarp)	1.7	2.7	10.8	7.6	11.5	4.9	6.3	6.0	8.4	37.0	34.8	34.7	40.8	2.7	4.0	5.1	6.3	3.4	3.7451
218115_at	NM_018154.1	FLJ10604	0.9	2.2	2.4	1.5	0.9	1.8	2.1	1.3	1.1	10.5	9.1	6.7	7.7	1.1	1.2	2.2	2.1	1.7	3.7435
215652_at	AK024382.1	FLJ14320	0.2	0.1	2.0	0.3	1.6	0.3	0.3	1.2	0.7	5.5	4.5	3.4	2.5	0.1	0.3	1.0	0.9	0.2	3.7249
212561_at	AA349595	RA86 interacting protein 1	10.0	6.1	10.2	12.4	11.4	18.7	14.9	12.1	10.0	66.3	60.0	47.6	37.1	4.0	8.7	9.9	13.9	5.9	3.6962
204166_at	NM_014963.1	KIAA0963	3.6	0.4	1.1	0.0	0.1	1.0	1.3	0.1	0.8	11.8	12.5	4.0	2.9	0.3	0.9	1.7	1.7	1.2	3.6908
221874_at	AB037745.1	KIAA1324	0.3	0.3	0.7	1.1	0.3	0.8	0.8	0.7	0.5	9.1	5.1	5.1	1.2	0.9	1.1	0.7	0.5	0.6	3.6808
217207_s_at	AK025267.1	butyrophilin like receptor	1.2	1.1	1.4	2.1	1.7	1.2	1.9	0.6	2.4	10.9	3.4	7.2	6.1	1.5	1.7	1.6	0.9	1.5	3.6795
212579_at	AA868754	KIAA0650	1.3	1.6	5.3	9.8	15.5	7.3	7.8	11.3	8.3	32.8	42.9	40.0	39.7	2.0	5.4	5.7	3.1	10.5	3.6784
212657_s_at	AW083357	IL-1 receptor antagonist IL-1Ra (IL-1RN)	48.8	2.3	0.9	0.5	0.6	2.1	0.9	1.5	1.3	35.2	37.0	48.2	35.5	0.6	0.8	0.3	9.3	0.4	3.6759
202392_s_at	NM_014338.1	phosphatidylethanolamine decarboxylase arginase (ARG1)	3.4	2.7	6.2	11.7	6.8	3.4	4.7	5.4	4.7	32.8	31.0	22.0	32.3	0.8	1.6	1.4	4.2	1.4	3.6753
206177_s_at	NM_000045.2	LPS-induced TNF-alpha factor (LITAF)	0.5	1.3	2.2	0.4	0.6	0.9	0.8	7.2	0.7	3.9	4.3	8.1	5.0	1.1	0.1	0.4	0.6	0.7	3.6722
200706_s_at	NM_004862.1	PIG7	31.2	39.0	20.7	64.6	62.5	15.6	13.4	31.8	21.7	173.2	148.5	172.0	150.2	8.5	13.3	42.7	14.3	16.7	3.6696
212478_at	AL050139.1	FLJ13910	0	0.1	0.2	2.3	3.5	1.4	0.8	1.5	1.0	3.7	3.0	4.8	6.5	0.1	0.3	1.1	0.6	0.4	3.6623
218660_at	NM_003494.1	dysferlin	2.5	0.5	1.5	0.2	0.2	1.7	0.2	2.6	1.1	48.5	51.8	44.5	20.4	3.3	1.2	1.7	10.6	0.2	3.6616
211982_x_at	AL546600	exportin 6	9.8	6.7	14.9	31.8	27.8	24.6	24.0	34.0	24.0	107.2	101.1	86.6	90.2	6.6	17.5	17.4	9.6	11.5	3.6408
202748_at	NM_004120.2	guanylate binding protein 2, interferon-inducible (GBP2)	2.4	5.3	3.7	9.0	7.4	3.3	2.1	3.0	3.3	28.1	35.2	45.0	24.8	4.2	7.3	9.0	6.3	1.9	3.6111
220088_at	NM_001736.1	CSAREceptor	2.2	2.3	15.4	24.6	24.8	17.1	15.6	9.8	12.0	90.5	104.5	84.4	91.1	2.3	1.2	0.5	25.6	1.0	3.6036
202890_at	T62571	microtubule-associated protein 7	0.9	0.1	0.7	1.4	1.1	0.1	0.0	0.2	0.1	2.5	3.1	3.2	7.1	0.0	0.1	0.4	0.1	0.1	3.6032
220987_s_at	NM_030952.1	DKFZP434J037	1.4	0.3	3.9	4.9	4.7	9.6	9.3	14.1	11.7	43.0	35.6	57.8	57.6	5.3	4.7	4.8	11.1	13.3	3.5748

Fig. 6H

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C. Neutrophil (Ne)-selective transcripts (6/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Bo 1	Bo 2	Bo 3 (small)	Bo 4 (small)	Ne 1	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	NeSL
207072_at	NM_003853.1	interleukin 18 receptor accessory protein (IL18RAP)	59	0.9	2.2	3.4	4.1	7.2	1.6	2.8	1.7	13.4	9.7	20.9	5.6	2.4	2.8	3.1	0.4	1.6	0.3	35722
215719_x_at	X83493.1	CD95, Fas, APO-1	1.0	0.6	3.1	2.7	1.6	2.2	5.2	1.8	1.7	19.0	31.9	11.4	9.4	1.0	4.5	2.2	1.6	1.1	4.4	35657
218404_at	NM_013322.1	sorting nexin 10	4.9	1.2	2.6	5.0	3.7	0.7	0.1	2.1	0.7	28.5	31.8	34.8	33.8	0.3	1.2	1.9	9.0	6.5	0.3	3563
219394_at	NM_024419.1	phosphatidylglycerophosphate synthase (PGS1)	3.4	3.0	1.7	4.2	3.5	2.4	3.8	6.1	9.2	17.2	16.9	17.5	16.3	1.0	2.1	2.6	2.4	1.5	1.7	35544
216913_s_at	AK021460.1	KIAA0690	0.1	0.3	0.1	0.1	0.1	1.9	2.5	2.3	2.8	8.9	8.3	7.5	10.9	0.1	0.1	0.2	2.5	0.1	0.0	35402
205118_at	M60626.1	formylpeptide receptor 1	0.1	0.2	0.8	0.1	1.1	0.1	0.4	0.6	0.1	3.9	7.0	3.2	7.8	0.2	0.1	0.1	1.4	0.1	0.0	35295
210564_x_at	AF009619.1	FLAME-1-delta	1.4	1.5	5.3	6.6	7.0	4.3	4.2	5.9	3.5	21.2	30.3	18.4	19.6	2.1	2.9	4.0	4.6	3.0	1.8	35148
213607_x_at	BE551347	KIAA0134	1.3	1.3	2.9	2.0	1.7	8.7	15.8	3.5	4.3	42.7	42.5	11.1	15.3	0.6	1.3	1.9	6.2	1.7	0.9	3514
203888_at	NM_000361.1	thrombomodulin	0.9	0.6	0.1	0.1	0.3	0.2	0.4	0.8	0.1	6.1	6.4	4.6	0.2	0.3	0.3	0.1	0.6	0.5	0.1	35126
210233_at	AF167343.1	interleukin-1 receptor accessory protein (IL1RAP)	0.5	0.1	0.0	0.1	0.6	0.8	0.4	0.6	0.7	1.8	3.0	2.0	2.3	0.6	0.0	0.0	0.0	0.0	0.3	35023
204959_at	NM_002432.1	myeloid cell nuclear differentiation antigen	1.2	0.6	24.2	50.0	26.2	17.5	17.9	49.8	22.3	249.8	290.2	186.0	217.0	3.4	1.6	0.6	66.6	2.5	0.0	34903
217967_s_at	AF288391.1	niban	6.3	3.7	16.3	42.4	35.9	27.9	29.5	43.0	30.9	107.4	115.3	117.9	110.3	2.6	7.5	9.9	4.9	3.4	20.4	34847
221763_at	A1694023	thyroid hormone receptor interactor 8	0.8	1.5	1.9	4.6	5.5	5.5	6.9	9.9	9.0	28.3	32.9	34.0	42.7	1.1	3.7	4.1	5.1	9.8	3.0	34777
207857_at	NM_006866.1	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain) member 2 (LILRA2)	0.4	0.5	3.6	8.5	5.3	4.5	4.9	1.6	6.3	33.5	34.3	46.2	50.8	1.8	0.0	0.1	11.6	0.5	0.1	34773
220740_s_at	NM_005135.1	solute carrier family 12 member 6 (SLC12A6)	1.6	1.0	2.5	3.3	3.4	3.5	5.6	3.2	3.2	12.6	19.0	10.7	14.4	4.0	2.9	2.2	2.9	3.5	0.8	34722
217739_s_at	NM_005746.1	pre-B-cell colony-enhancing factor	7.1	1.7	9.9	46.0	61.0	18.9	13.9	12.9	9.3	112.4	120.5	90.8	93.4	1.2	2.3	1.4	17.6	2.1	3.1	34242
205041_s_at	NM_000607.1	orosomucoid 1 (ORM1)	0.3	1.0	0.4	0.1	0.1	0.0	0.1	1.0	0.1	2.6	3.6	2.7	0.4	0.1	0.2	0.1	0.5	0.0	0.1	34189
214784_x_at	BE966299	exportin 6	7.4	5.0	10.0	23.7	23.9	13.0	16.7	23.3	20.5	60.3	67.8	57.2	60.8	2.9	8.7	7.8	6.6	5.9	5.4	34155
217985_s_at	AA102574	bromodomain adjacent to zinc finger domain, 1A	1.5	1.4	1.8	2.6	3.8	7.4	5.1	7.3	4.7	16.9	19.2	22.1	24.2	2.7	2.5	2.3	3.5	2.4	0.9	33999
212598_at	A1806395	KIAA0993	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	5.5	7.3	3.1	3.2	0.2	0.1	0.0	1.0	0.1	1.3	33933
219053_s_at	NM_017966.1	FLJ20847	2.6	2.0	1.9	2.3	2.3	2.6	2.1	3.0	2.8	11.3	7.6	22.2	34.1	1.6	0.5	0.9	4.7	1.3	2.9	33686
217475_s_at	AC002073	PAC clone RP3-S15N1	0.6	0.5	0.6	0.2	0.4	1.3	1.3	0.5	1.2	5.9	9.8	1.6	1.4	0.7	0.3	0.1	0.5	0.7	0.2	33448
46323_at	AL120741	Ca2+-dependent endoplasmic reticulum nucleoside diphosphatase	4.4	3.2	4.2	8.3	7.2	5.3	6.7	11.4	7.9	20.0	21.5	33.9	26.3	2.5	2.8	3.6	4.3	3.4	5.0	33028
201965_s_at	NM_015046.1	KIAA0625	2.7	3.1	3.3	8.5	8.3	4.9	5.8	7.4	7.5	19.5	18.5	18.7	27.8	2.2	3.9	3.4	4.6	5.6	2.6	33019
203628_at	NM_000875.2	insulin-like growth factor 1 receptor	0.5	0.1	3.7	3.0	4.0	6.8	4.9	2.7	5.8	18.8	23.4	6.8	20.6	1.6	0.1	2.8	2.4	2.0	3.5	32989
202193_at	NM_005569.2	LIM domain kinase 2 (LIMK2)	1.8	1.5	1.9	5.6	5.6	6.4	4.8	11.3	8.9	17.0	20.5	36.5	28.2	0.1	1.3	1.1	0.6	0.5	0.8	32887
203042_at	NM_002294.1	transcript variant 2a	2.4	3.1	1.1	1.7	1.3	5.9	6.4	12.4	10.7	21.3	27.0	44.1	35.4	0.8	0.6	0.5	3.2	0.8	9.4	3282
220326_s_at	NM_018071.1	lysosomal-associated membrane protein 2 (LAMP2)	5.1	4.5	1.9	1.2	1.9	6.3	8.9	5.2	8.5	25.3	28.1	19.2	21.0	0.9	0.1	0.7	6.4	0.1	4.1	32759
212470_at	AB011088.1	FLJ10357	4.0	2.9	3.3	6.3	7.2	4.5	4.0	4.7	4.9	13.2	17.0	18.1	24.0	1.2	2.5	2.2	3.9	3.0	5.4	32688
211133_x_at	AF009643.1	sperm associated antigen 9	1.9	1.4	0.8	1.5	1.3	3.1	2.7	3.8	2.1	42.1	42.2	27.0	25.1	2.7	0.9	0.5	10.2	0.4	0.2	32526
219313_at	NM_017577.1	clone 6 immunoglobulin-like transcript 5	0.0	0.8	0.2	0.0	0.4	0.2	0.1	0.1	0.0	3.8	3.7	3.1	5.6	0.2	0.1	0.1	0.0	1.2	0.1	32404
221149_at	NM_018485.1	DKFZp434C0328	0.2	0.1	0.8	0.7	1.2	0.7	0.9	0.9	0.6	3.3	3.2	4.2	2.9	0.0	0.3	0.2	1.0	0.1	0.3	32282
203433_at	NM_006441.1	G protein-coupled receptor GRP77	1.4	1.8	1.5	2.5	1.6	3.1	4.2	3.5	3.1	15.8	11.4	9.6	9.0	1.6	1.8	1.9	2.9	1.7	1.5	32181
214486_x_at	AF041459.1	5, 10-methylenetetrahydrofolate synthetase	1.9	2.1	10.7	5.0	6.5	4.2	5.3	4.3	6.0	26.3	16.2	25.3	24.2	2.4	3.7	5.0	5.3	2.3	1.9	32114
		FADD-like apoptosis regulator																				

Fig. 6l

C. Neutrophil (Ne)-selective transcripts (7/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba.S.I.
209222_s_at	BC000296.1	oxysterol binding protein-like 2	1.3	0.2	2.7	8.8	8.0	5.4	5.4	7.7	7.3	17.2	18.4	22.3	23.9	0.9	2.3	3.4	2.8	2.0	1.3	3.1877
202334_s_at	AA877765	ubiquitin-conjugating enzyme E2B	3.3	3.4	4.8	15.5	12.1	5.3	7.2	14.7	12.8	20.9	25.6	43.6	38.1	4.0	4.5	3.9	2.5	4.9	4.6	3.1871
203266_s_at	NM_003010.1	mitogen-activated protein kinase	3.7	2.4	4.9	8.2	6.3	2.5	4.8	6.8	5.0	14.7	15.2	27.4	26.9	2.8	2.4	2.6	2.7	2.3	2.7	3.1804
58780_s_at	R42449	kinase 4	4.5	5.4	1.5	3.9	3.0	7.8	9.6	12.8	16.4	28.0	27.6	46.7	44.1	1.2	0.6	0.1	6.5	0.2	5.7	3.1803
210582_s_at	AL117466.1	FLJ10357	3.8	1.9	4.3	5.1	4.8	8.7	10.3	10.8	9.4	33.9	36.5	30.8	23.8	1.3	1.7	1.8	1.9	0.9	1.4	3.1609
214766_s_at	AL080144.1	LIM domain kinase 2	1.3	0.2	2.0	3.1	4.2	1.9	1.4	2.1	2.4	9.4	9.5	9.9	11.3	3.2	1.3	0.8	0.5	1.0	1.3	3.1414
202266_at	NM_016614.1	ELYS transcription factor-like protein	9.8	6.2	9.4	23.7	20.9	8.6	9.9	16.5	14.0	36.1	56.5	64.5	57.5	4.5	7.7	9.4	5.3	8.2	6.3	3.1402
203278_s_at	NM_016621.1	TM6SF2	2.1	2.8	2.7	14.8	11.0	5.7	5.0	7.4	4.9	21.0	16.6	31.0	30.6	0.7	3.0	4.5	3.1	2.7	3.0	3.1382
207291_at	NM_024081.1	TRAF and TNF receptor-associated protein (AD022)	0.1	1.2	1.3	1.4	1.1	0.9	0.2	0.4	0.2	3.8	7.9	4.5	8.5	0.2	0.8	0.1	1.9	1.1	0.4	3.1336
213229_at	BF590131	gamma-carboxyglutamic acid	8.5	4.5	19.5	12.9	15.4	15.9	9.7	19.1	16.0	35.2	39.0	61.4	69.4	6.2	5.9	7.3	15.2	12.2	5.0	3.1306
204204_at	NM_001860.1	Dicer1, Dcr-1 homolog (Drosophila)	1.7	1.7	7.3	0.3	0.8	1.7	0.9	2.3	1.2	22.6	23.8	31.3	36.0	2.0	1.2	1.2	8.9	0.2	0.4	3.1262
201364_s_at	AF242521.1	solute carrier family 31	8.3	7.3	4.4	2.2	1.9	11.5	21.9	8.0	7.7	61.9	59.1	21.0	27.7	2.2	5.1	6.3	12.2	6.2	9.6	3.1253
210784_x_at	AF009634.1	ornithine decarboxylase antizyme	1.4	0.1	2.1	1.2	2.4	2.5	2.2	2.8	2.1	52.1	48.8	31.8	36.3	0.8	0.2	0.2	13.3	0.3	0.2	3.1236
202625_at	AI356412	clone 17.6 immunoglobulin-like	6.9	6.9	5.0	18.2	14.9	20.7	21.7	27.7	28.6	74.7	76.3	77.5	75.7	7.5	1.7	0.9	17.1	23.6	0.5	3.1131
221895_at	AW469184	transcript	2.2	0.5	5.4	5.2	5.8	5.2	3.4	7.6	5.1	14.8	12.0	24.6	19.2	2.0	2.4	2.1	5.2	1.5	1.6	3.11
37384_at	D13640	v-yes-1 Yamaguchi-sarcoma viral related oncogene homolog (LYN)	2.5	3.0	3.4	3.8	3.8	6.7	6.6	7.6	6.6	25.2	17.9	21.3	29.4	2.6	2.5	2.5	7.4	1.8	2.8	3.0985
206608_s_at	NM_020366.1	major histocompatibility complex, class I, B	1.1	1.4	1.2	0.8	1.0	1.1	1.0	0.5	1.4	6.1	3.4	5.3	4.7	1.5	0.9	0.8	1.3	0.5	0.7	3.091
204924_at	NM_003264.1	retinitis pigmentosa GTPase regulator interacting protein 1	1.8	0.1	2.1	8.2	7.6	2.8	0.4	0.8	1.4	52.9	88.0	94.4	99.8	1.6	1.3	0.1	26.3	0.9	0.4	3.0909
204781_s_at	NM_000043.1	regulator of G-protein signaling 1	2.0	1.1	5.9	11.0	8.9	5.4	4.4	6.8	7.0	20.6	27.1	27.0	29.1	0.3	5.2	5.3	4.0	2.0	3.8	3.0827
212606_at	AI806395	CD95, Fas, APO-1	2.0	2.0	0.0	0.7	0.6	0.7	0.0	0.1	0.1	18.0	14.3	25.0	26.9	0.1	0.2	0.3	6.6	0.0	3.4	3.0797
211316_x_at	AF009616.1	KIAA0993	3.1	2.9	20.1	19.4	31.9	11.6	11.9	20.6	19.1	58.8	74.1	72.8	81.0	4.1	6.8	8.7	10.3	5.5	2.6	3.0752
203045_at	NM_004148.1	FLAME-1	4.4	2.5	3.2	6.4	4.8	10.7	9.7	18.5	12.1	29.3	34.1	44.7	46.1	0.5	1.2	1.7	8.3	0.2	2.9	3.0746
204949_at	NM_002162.2	ninjurin 1	3.0	3.7	5.7	46.3	34.5	38.9	51.6	94.5	93.7	161.1	168.3	239.1	241.1	4.5	13.6	21.0	17.6	19.9	1.3	3.0617
206208_at	NM_000717.2	intercellular adhesion molecule 3	0.2	0.6	0.1	0.1	0.1	1.1	0.7	1.0	0.8	5.6	5.2	2.8	2.4	1.2	0.1	0.1	0.1	0.1	0.1	3.0572
213727_x_at	AI743654	(ICAM3)	2.1	1.7	5.0	15.0	12.1	8.9	13.7	25.4	23.9	49.9	28.3	59.9	75.8	0.7	4.5	6.6	5.7	5.4	3.7	3.0554
202626_s_at	NM_002350.1	carbonic anhydrase IV (CA4)	15.5	9.5	12.1	12.7	14.8	32.6	31.6	54.0	41.0	110.1	115.1	122.7	127.2	18.4	2.1	1.5	36.8	33.0	0.6	3.0541
206420_at	NM_005849.1	metallophosphoesterase	1.1	0.3	0.2	0.4	0.7	1.9	1.2	1.1	1.0	17.5	24.2	30.6	33.3	1.4	0.4	0.4	8.4	0.3	0.3	3.0442
201651_s_at	NM_007229.1	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN)	21.4	17.4	4.6	24.8	20.1	13.3	19.5	33.9	35.3	61.3	72.5	76.1	94.4	24.7	4.9	4.4	8.6	6.1	8.0	3.0391
219540_at	AU150728	immunoglobulin superfamily, member 6 (IGSF6)	2.0	1.0	1.3	3.7	3.6	2.0	1.5	4.4	3.7	6.7	6.9	9.2	9.9	1.0	2.1	1.3	1.0	1.6	0.1	3.0361
201244_s_at	NM_002880.1	protein kinase C and casein kinase substrate in neurons 2 (PACSIN2)	6.0	5.4	12.4	32.8	33.1	14.9	19.0	27.3	25.7	60.4	58.2	89.2	86.2	2.2	6.6	11.3	12.8	7.6	7.3	3.0329
203265_s_at	AA810268	zinc finger protein 267	1.4	1.2	2.8	6.4	4.5	1.7	2.6	3.5	3.1	12.8	12.8	10.4	16.8	1.4	1.4	1.3	1.3	2.5	1.5	3.028
203030_s_at	AF007555.1	v-rat-1 murine leukemia viral oncogene homolog 1 (RAF1)	0.0	0.0	1.6	1.2	0.1	0.1	0.1	0.1	0.1	0.8	3.0	1.1	2.8	0.1	0.1	0.0	0.1	0.0	0.0	3.0269
203739_at	NM_006526.1	mitogen-activated protein kinase kinase 4	1.9	2.6	3.0	18.4	8.4	7.6	8.0	14.7	14.9	37.3	45.1	24.4	27.0	1.2	4.6	5.3	6.1	5.5	3.6	3.0158
204747_at	NM_001549.1	IAR receptor-like protein-tyrosine phosphatase	2.0	3.0	4.9	6.0	3.5	4.3	12.4	4.4	3.0	24.2	27.0	15.4	12.0	0.3	1.8	1.2	6.2	1.4	2.6	3.0143
206209_s_at	NM_000717.2	zinc finger protein 217	0.7	1.0	0.8	0.6	0.6	2.2	2.1	1.5	2.1	13.8	7.4	4.7	3.5	2.1	1.0	0.5	0.9	1.0	0.5	3.0112
		interferon-induced protein with tetrapeptide repeats 4 (IFIT4)																				
		carbonic anhydrase IV (CA4)																				

Fig. 6J

D. Mast cell (MC)-selective transcripts (1/2).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 Eo (small)	Eo 2 (small)	Eo3 (small)	Eo4 (small)	Ne 1 (small)	Ne 2 (small)	Ne3 (small)	Ne4 (small)	pI	CD4	CD8	CD14	CD19	Fb	MCSL
217023_x_at	AF099143	tryptase beta	169.4	118.7	0.7	1.1	0.4	0.1	0.5	0.1	0.2	0.1	0.6	0.4	0.3	0.1	0.1	0.2	0.1	0.2	202.148
215382_x_at	AF206666.1	tryptase beta	168.1	108.4	1.7	0.7	0.4	0.2	0.2	0.1	0.1	0.3	0.1	0.1	0.7	0.1	0.1	0.1	0.1	0.5	172.668
204041_at	NM_000898.1	monoamine oxidase B	23.5	46.9	0.2	0.7	0.1	0.1	0.2	0.6	0.3	0.1	0.2	0.1	0.2	0.2	0.1	0.2	0.1	0.2	136.311
210084_x_at	AF206665.1	tryptase alpha	131.1	92.3	0.7	1.2	1.2	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.6	0.1	0.0	0.1	0.1	0.1	112.376
216474_x_at	AF206667.1	tryptase beta	210.0	120.9	2.4	2.0	1.4	1.2	0.2	0.1	0.2	1.1	0.1	0.1	1.8	0.8	0.9	0.9	0.1	0.1	84.3375
205683_x_at	NM_003294.2	tryptase beta	195.5	95.3	2.4	2.7	0.3	0.2	0.2	0.6	0.4	0.1	0.4	1.0	2.0	0.7	0.2	0.3	0.2	0.1	67.2617
207741_x_at	NM_003293.2	tryptase alpha	175.0	99.7	2.2	2.2	1.8	0.5	0.2	0.3	0.2	0.2	0.3	0.3	2.2	0.7	0.1	0.5	0.3	0.6	59.015
207134_x_at	NM_024164.2	tryptase beta	214.6	112.3	3.1	3.8	1.7	1.2	0.3	0.8	0.6	0.3	0.8	0.4	0.1	0.5	0.2	1.1	0.4	0.2	57.1834
205653_at	NM_001911.1	cathepsin G	91.2	57.0	2.7	1.1	0.9	0.9	0.4	3.1	0.8	0.3	1.4	1.6	0.6	0.7	0.2	1.3	0.3	0.2	51.4749
205266_at	NM_002309.2	leukemia inhibitory factor	17.0	9.8	0.2	0.2	0.3	0.3	0.1	0.2	0.2	0.1	0.2	0.4	0.7	0.1	0.2	0.1	0.1	0.1	44.3659
210324_at	M17263.1	complement protein C8 gamma	2.9	6.9	0.1	0.1	0.0	0.0	0.0	0.1	0.1	0.3	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	33.806
211743_s_at	BC005929.1	major basic protein	74.3	70.7	1.0	4.7	2.7	0.1	0.7	0.8	0.6	0.2	0.3	0.7	0.2	0.1	0.2	0.3	0.2	0.3	31.5959
211549_s_at	U63296.1	15-hydroxyprostaglandin dehydrogenase	48.3	21	2.5	2.5	1.4	1.5	1.3	0.8	0.9	0.1	0.1	0.2	0.1	1.1	0.5	0.8	0.5	0.0	24.8454
206726_at	NM_014485.1	prostaglandin D2 synthase	119.0	94.0	5.0	7.8	5.7	0.7	0.1	1.0	0.5	0.2	0.2	0.2	0.6	1.3	0.7	1.2	0.3	0.0	17.432
205011_at	NM_014622.1	loss of heterozygosity, 11, chromosomal region 2, gene A	76.1	70.9	3.0	6.8	4.5	2.3	1.0	1.4	1.9	0.2	1.1	1.2	1.8	2.9	2.2	1.3	1.7	2.0	16.2511
205428_s_at	NM_001740.2	calbindin 2	16.7	63.4	1.3	0.7	0.9	0.4	1.6	0.7	1.3	1.8	1.6	3.6	1.5	1.7	0.7	1.1	0.6	0.9	16.1621
219255_at	NM_024554.1	FLJ11413	10.0	9.2	0.1	0.1	0.1	0.2	0.1	0.6	0.6	0.1	0.6	0.1	0.2	0.1	0.6	0.1	0.0	0.2	15.639
204468_s_at	NM_005424.1	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	3.6	2.8	0.5	0.3	0.1	0.0	0.1	0.2	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	14.4259
208343_s_at	AF146343.1	CYP7A promoter binding factor	1.5	0.9	0.0	0.0	0.3	0.1	0.0	0.1	0.0	0.1	0.0	0.2	0.4	0.1	0.0	0.0	0.0	0.0	13.8025
205051_s_at	NM_000222.1	CD117 c-KIT	92.1	85.8	6.2	8.1	7.3	2.3	5.2	6.5	2.7	0.7	2.1	0.8	1.1	0.8	0.2	0.5	0.1	0.5	12.3815
210102_at	BC001234.1	loss of heterozygosity, 11, chromosomal region 2, gene A	40.9	41.1	2.8	3.7	4.5	0.3	0.4	0.3	0.6	0.7	0.9	0.2	0.6	1.8	0.8	0.7	1.2	0.6	11.3619
210796_x_at	D86359.1	siatic acid binding lg-like lectin, siglec6	17.8	26.0	1.5	1.0	1.1	1.2	1.5	1.3	1.4	1.4	2.3	1.7	1.3	2.0	1.4	1.5	1.8	1.0	10.5398
206519_x_at	D86358.1	siatic acid binding lg-like lectin, siglec6	3.4	7.9	0.0	0.3	0.4	0.0	0.0	0.0	0.1	0.0	0.1	0.5	0.2	0.5	0.0	0.0	0.4	0.0	10.13
206480_at	NM_000897.1	leukotriene C4 synthase	8.8	16.0	0.3	0.2	0.6	2.4	1.6	0.5	0.1	0.2	1.1	0.1	0.1	1.3	0.1	0.3	0.1	0.1	9.27381
206617_s_at	NM_002910.4	renin-binding protein	10.6	6.2	1.2	0.1	0.4	2.8	1.6	0.5	0.1	0.6	2.1	0.1	0.1	0.9	0.2	0.7	0.3	0.4	9.18529
208089_s_at	NM_030794.1	tudor domain containing 3	6.0	13.4	0.8	0.6	0.2	0.5	0.7	0.5	0.5	0.1	0.6	0.3	0.0	0.7	0.7	1.1	0.8	0.6	8.16897
205466_s_at	NM_005114.1	heparan sulfate 3-D-sulfotransferase ADAMTS3 a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3	18.1	7.2	0.1	0.4	0.1	0.7	0.1	0.3	0.2	0.4	0.1	0.8	0.4	0.1	0.0	0.0	0.2	1.4	8.15381
214913_at	AB002364.1	tissue-plasminogen activator	6.8	4.3	0.5	0.7	0.8	0.5	0.7	0.6	0.4	0.5	0.4	0.7	1.2	0.7	0.6	0.5	0.5	0.5	7.2214
201860_s_at	NM_000930.1	siatic acid binding lg-like lectin, siglec6	22.2	29.7	0.2	0.4	0.1	0.1	0.3	0.5	0.5	0.1	0.1	1.3	0.4	1.6	0.1	0.2	0.6	0.1	7.10135
206520_x_at	NM_001245.1	LR8 protein	19.0	22.7	2.4	1.1	0.8	1.1	1.5	1.3	1.0	2.0	2.0	0.4	1.4	2.9	2.1	2.3	1.9	1.2	7.10132
220532_s_at	NM_014020.1	FLJ10305	52.4	18.2	0.8	0.8	1.0	6.4	2.9	1.5	1.2	0.4	0.3	1.4	0.6	2.2	0.6	0.2	5.0	0.1	6.1662
218169_at	NM_018052.1	nuclear receptor subfamily 1, group 1, member 3	6.2	14.6	0.3	0.2	0.4	0.4	0.3	0.3	0.4	0.6	0.5	0.1	0.1	0.5	0.2	1.4	1.6	0.3	6.04597
221728_x_at	AK025198.1	tudor domain containing 3	5.6	5.5	0.6	0.9	1.0	0.4	0.3	0.9	0.8	0.7	0.6	1.4	0.9	0.9	0.8	0.7	0.7	0.8	5.70228
214028_x_at	AU156998	lipase	3.2	11.9	0.9	0.0	0.4	0.8	0.3	0.4	0.7	0.6	0.6	0.1	0.1	0.8	1.2	1.1	0.1	0.7	5.10738
221552_at	BC001698.1	MKP-1 like protein tyrosine phosphatase (MKP-1)	10.6	3.4	0.9	1.8	1.1	0.9	1.1	1.0	0.9	0.2	0.2	0.7	0.1	0.1	0.2	0.7	0.9	0.3	5.02434
203367_at	NM_007026.1	heparan sulfate 6-O-sulfotransferase	15.0	45.4	1.2	0.9	0.8	0.9	0.9	0.8	0.1	0.2	0.7	0.4	2.0	0.9	1.0	2.7	0.5	1.4	5.00514
206997_s_at	NM_004807.1		4.2	3.8	0.2	0.1	0.1	0.4	0.4	0.1	0.3	0.3	0.4	0.3	0.7	0.3	0.2	0.6	0.3	0.8	4.81127

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Fig. 6K

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D. Mast cell (MC)-selective transcripts (2/2).

Probeset	Accession #	Transcripts	MC																				
			cord blood	lung	MC	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl CD4	CD8	CD14	CD19	Fb	MCs.I.	
207480_s_at 45288_at	NM_020149.1 AA209239	TALE homeobox protein Meis2e lipase	14.0 10.9	14.9 3.0	1.9 0.2	3.6 2.1	4.0 0.8	1.7 0.5	1.9 0.5	5.3 1.3	3.8 0.9	0.3 0.1	0.6 0.1	1.0 0.2	0.3 0.1	0.5 0.4	0.8 0.5	0.4 0.5	0.6 1.3	0.4 1.0	0.8 0.9	4.72642 4.52869	
207039_at 201650_at 214533_at	NM_000077.1 NM_002276.1 NM_001836.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) keratin 19 chymase	7.5 6.2 10.1	3.6 12.0 2.7	0.7 0.0 0.4	0.7 0.0 0.2	0.1 0.3 0.8	0.6 0.1 0.1	0.4 0.0 0.1	0.3 0.0 0.8	0.5 0.0 0.6	0.1 0.0 0.6	1.2 0.1 0.1	0.6 0.1 0.2	1.1 0.1 0.2	0.1 0.1 0.2	0.9 0.0 0.7	0.5 0.1 0.5	0.8 0.1 1.0	0.1 0.0 0.4	1.2 2.0 0.3	4.35629 4.35547 4.27984	
218211_s_at 203916_at	NM_024101.1 NM_003635.1	melanophilin N-deacetylaseN-sulfotransferase	24.8 17.9	29.6 26.7	2.7 3.2	2.5 6.5	1.8 6.8	3.0 2.5	2.5 2.7	1.9 3.6	2.2 3.1	4.6 4.2	4.1 3.4	3.3 5.5	4.1 5.2	6.4 0.9	4.0 3.1	3.2 4.9	2.4 3.3	3.4 2.7	2.7 2.4	4.24499 4.20693	
212336_at 200766_at 202218_s_at 204066_s_at	AB002336.1 NM_001909.1 NM_004265.1 NM_014914.1	erythrocyte membrane protein band 4.1-like 1 cathepsin D delta-6 fatty acid desaturase (FADS6) centaurin, gamma 2	3.8 42.6 18.8 5.3	6.4 39.5 24.5 7.9	0.1 2.5 0.4 0.4	0.2 5.3 0.2 0.4	0.1 4.3 1.0 0.7	0.5 4.3 0.3 0.2	0.1 4.8 0.1 0.2	0.2 3.4 0.8 0.6	0.4 2.7 0.5 0.6	0.1 4.0 0.2 0.3	0.1 6.7 0.1 0.5	0.1 3.1 0.1 0.4	0.5 1.9 0.1 0.4	0.1 2.6 1.6 0.8	0.4 1.6 0.1 0.6	0.2 2.5 0.6 1.6	0.4 10.0 0.1 0.6	0.4 1.6 0.5 1.0	1.2 5.9 5.3 1.6	4.12758 4.1037 4.08548 4.06712	
209644_x_at 221679_s_at 211538_s_at 211548_s_at	U38945.1 AF225418.1 U56725.1 J05594.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) lipase heat shock protein 70kD 15-hydroxyprostaglandin dehydrogenase	14.0 2.8 4.4 82.6	6.4 1.9 7.4 60.0	1.0 0.4 0.3 19.4	1.4 0.9 0.6 26.0	0.7 0.1 0.4 16.3	1.2 0.3 0.6 3.2	1.3 0.4 0.3 2.9	1.7 0.4 0.3 1.8	1.5 0.1 0.9 1.7	1.0 0.1 1.4 0.8	1.6 0.5 0.4 0.5	1.5 0.0 1.0 0.9	2.1 0.5 0.8 0.2	2.3 0.1 1.5 4.1	1.8 0.1 0.5 1.2	1.5 0.6 0.5 0.9	0.9 0.6 0.1 0.1	0.3 0.5 0.7 0.6	0.2 2.4 0.7 0.2	3.88459 3.83039 3.80423 3.49258	
210174_at 219412_at	AF228413.1 NM_022337.1	member 2 RAB38, member RAS oncogene	2.9 3.9	3.4 4.0	0.5 0.1	0.5 0.4	0.6 0.3	0.8 0.7	1.1 0.1	0.7 0.2	1.2 0.3	1.1 0.2	0.4 0.2	0.1 1.1	0.4 0.2	0.9 0.7	0.7 0.2	0.2 0.8	0.2 0.4	0.6 0.1	0.3 0.5	3.47124 3.32805	
201850_at 205888_s_at	NM_001747.1 A1962693	gelsolin-like capping protein (actin filament) KIAA0555	70.5 5.4	64.5 4.6	9.6 0.7	30.8 1.6	28.8 1.2	8.1 0.8	7.8 0.7	11.5 0.1	9.9 1.0	2.6 1.3	3.6 0.3	3.0 0.2	2.4 0.6	1.6 1.2	1.1 0.3	1.0 1.5	17.0 0.7	5.8 1.2	5.3 0.4	3.29919 3.25197	
221750_at	BG035985	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	5.0	3.8	0.9	1.5	1.1	1.1	1.2	1.3	1.0	1.3	0.5	0.7	1.2	0.7	0.5	1.1	0.7	1.4	1.2	3.1926	
214218_s_at 218788_s_at	AV699347 NM_022743.1	nuclear receptor subfamily 1, group I, member 3 FLJ21080	3.5 16.1	3.5 23.7	0.7 0.5	0.6 2.3	0.7 2.5	0.5 0.9	2.2 1.1	0.5 2.7	0.7 2.1	1.2 1.1	1.0 1.0	0.6 0.8	1.1 0.9	0.9 2.3	0.9 2.1	0.3 2.9	0.6 0.6	0.8 2.0	0.4 6.3	3.15254 3.07851	
218087_s_at 221577_x_at 35820_at 208744_x_at	NM_015385.1 AF003934.1 X62078 BG403660	SH3-domain protein 5 (ponsin) prostate differentiation factor GM2 activator protein heat shock 105kD	1.4 7.8 21.8 7.3	1.9 5.5 17.6 4.8	0.4 0.6 1.4 0.5	0.9 0.3 3.3 0.2	0.4 0.5 1.3 0.2	0.5 0.6 0.3 0.9	0.0 0.1 0.3 0.1	0.0 0.2 0.2 0.4	0.1 0.6 0.5 0.6	0.1 0.0 0.5 0.1	0.1 0.2 0.8 0.1	0.1 0.3 1.9 0.3	0.1 0.1 0.4 0.8	0.0 0.2 0.2 1.7	0.2 0.0 0.2 0.2	0.2 0.1 6.5 2.0	0.2 0.1 5.0 0.9	0.1 2.1 2.7 0.9	0.366 3.05532 3.01647 3.00671		

Fig. 6L

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E. Basophil and eosinophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC	cord	Ba1	Ba2	Ba3	Eo	Eo3	Eo4	Ne	Ne3	Ne4	CD4	CD8	CD14	CD19	Fb	Ba+Po SL
211517_s_at	M96651.1	IL-5R interleukin 5 receptor alpha	0.6	0.1	118	282	179	164	326	295	0.0	0.7	1.0	0.0	0.4	0.2	0.0	0.2	61956
210744_s_at	M75914.1	IL-5R interleukin 5 receptor alpha	0.2	1.6	154	308	153	187	297	330	0.3	0.2	0.5	0.1	0.1	0.1	0.2	0.1	42811
206361_at	NM_004778.1	CRTH2 chemotactant	1.8	0.3	220	405	153	337	389	423	1.0	2.6	2.1	0.8	1.4	1.0	1.2	0.9	16642
206207_at	NM_001828.3	receptor-homologous molecule expressed on Th2 cells	1.1	0.1	2700	219.1	2036	2268	179.7	163.1	2.1	194	493	2.8	1.0	1.4	0.9	0.7	15164
203638_s_at	NM_022969.1	Charcot-Leyden crystal protein	0.2	0.1	73	435	330	4.1	123	233	0.1	0.1	0.3	0.1	0.1	0.2	0.1	0.1	13357
207111_at	NM_001974.1	fibroblast growth factor R2	1.5	0.1	164	495	345	85.9	93.1	935	2.7	3.7	5.1	34	1.7	0.8	7.1	1.6	80092
215248_at	AU145003	egf-like module containing, mucin-like hormone receptor-like sequence 1 (EMR-1)	0.7	0.3	5.7	4.7	52	45	2.1	2.1	1.0	0.1	0.1	0.2	0.1	0.1	0.1	0.2	72618
205471_s_at	AW772082	dachshund (Drosophila) homolog	0.1	0.6	5.1	4.1	37	64	83	76	0.8	0.9	0.8	0.1	0.1	0.3	0.5	0.0	68198
218857_s_at	NM_025080.1	Hs63931	1.0	7.0	180	353	186	137	125	154	1.3	1.7	1.9	0.3	0.5	0.4	2.4	0.2	65045
221169_s_at	NM_021624.1	FLJ22316	0.2	0.5	45	125	89	19	26	29	0.5	0.6	0.6	0.4	0.7	0.5	0.7	0.0	59783
201769_at	NM_014666.1	histamine receptor H4	7.8	9.1	41.7	1015	76.0	268	34.1	35.7	3.0	2.9	4.2	4.5	6.3	6.9	8.0	9.0	5.1015
208228_s_at	M87771.1	entrophin	0.3	1.4	3.7	102	83	39	45	83	0.8	1.4	1.1	1.3	0.4	0.7	0.3	0.5	49922
213605_s_at	AL049987.1	secreted fibroblast growth factor receptor (K-sam_III)	0.8	0.0	108	468	44.7	67	6.1	206	1.3	1.4	4.5	2.9	1.1	2.1	3.7	2.0	47426
205382_s_at	NM_001928.1	hypothetical protein, MNCb-4779	3.5	0.1	62.0	206.0	176.5	62.4	48.1	44.8	7.1	32.5	163	0.1	0.6	0.1	15.6	0.1	47202
49452_at	A057637	adipsin	0.6	0.2	52	7.7	6.6	6.9	5.9	10.2	1.1	0.2	0.3	0.1	1.6	1.6	0.5	1.3	47183
220307_at	NM_016382.1	hypothetical protein LOC283445	0.5	0.1	15.7	87.0	65.4	99	108	185	0.3	0.4	1.2	3.0	0.1	0.4	3.5	1.1	46297
210108_at	BE550599	CD244 natural killer cell receptor 2B4	0.2	0.1	1.0	1.7	2.4	0.9	0.8	1.8	0.0	0.6	0.5	0.0	0.3	0.1	0.0	0.3	45958
209193_at	M24779.1	calcium channel, voltage-dependent, L type, alpha 1D subunit	6.8	7.1	61.3	110.3	100.1	47.0	79.7	79.5	192	18.8	21.1	4.1	12.7	13.9	4.6	4.0	4.1983
202794_at	NM_002194.2	protein kinase-related oncogene (PLM1)	5.7	6.2	7.1	25.8	20.5	17.9	24.8	57.8	2.8	2.7	2.6	4.0	1.9	1.8	2.6	4.8	4.1158
208304_at	NM_001837.1	inositol polyphosphate-1-phosphatase (INPP1)	0.2	1.1	107.2	142.9	102.2	46.4	91.7	107.5	28.3	20.0	26.3	25.1	0.2	0.5	0.4	0.2	0.4
206111_at	NM_002934.1	CCR3 chemokine (C-C motif) receptor 3	2.2	2.0	33.7	71.4	38.4	104.7	80.8	45.1	2.0	2.3	3.1	2.8	1.4	0.7	0.4	0.7	0.5
43427_at	A1970898	eosinophil-derived neurotoxin	0.8	0.7	2.1	4.8	4.3	5.1	4.6	6.4	1.0	0.8	0.7	0.8	1.1	1.0	1.3	1.1	37554
213804_at	A1039084	hypothetical protein LOC283445	0.6	1.2	43	8.0	68	86	56	97	0.7	0.5	2.2	1.7	1.4	1.2	1.4	1.9	36088
209906_at	U62027.1	inositol polyphosphate-5-phosphatase, 75kD	12.4	11.2	44.1	72.3	50.5	18.8	38.8	299	1.2	1.2	1.8	3.8	1.6	1.6	3.0	0.6	36039
202804_at	A1539710	Ca receptor	8.5	7.0	242	562	48.9	142	20.0	207	3.0	3.6	4.3	6.0	3.8	3.5	5.4	5.5	35673
221675_s_at	AF195624.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	7.0	6.8	31.6	79.7	55.8	26.9	32.6	41.8	5.2	7.5	5.9	9.6	2.4	3.1	3.3	7.7	35626
201562_s_at	NM_003104.1	cholinephosphotransferase 1 beta	2.0	1.5	2.9	42	4.1	7.4	11.6	11.2	1.7	2.5	1.5	1.3	1.3	1.4	1.8	1.1	35098
210230_at	BC003629.1	sorbitol dehydrogenase (SORD)	1.1	0.1	8.3	11.0	13.3	2.4	5.1	4.1	0.1	0.5	0.2	0.7	0.3	0.2	0.6	0.8	32532
219919_s_at	NM_018276.1	FLJ23438 f5, clone HRC13275	0.1	0.2	3.1	1.8	2.5	1.7	4.3	2.1	0.1	0.5	0.4	0.3	0.1	0.1	0.1	0.1	32497
204301_at	NM_014867.1	FLJ10928	0.6	0.1	3.8	14.3	10.7	5.3	6.8	10.5	1.2	0.6	1.6	1.6	1.0	0.8	1.2	2.6	32398
210999_s_at	U66065.1	KAA0711	3.6	1.7	8.4	13.6	11.8	7.3	4.6	6.4	2.2	1.7	1.9	2.0	1.9	1.2	1.2	1.6	3.1044
209539_at	D25304.1	Grb 10- and Grb-IR-related splice variant 1	13.1	24.8	288	74.7	73.0	53.8	35.5	596	9.2	6.1	18.5	13.7	3.1	10.8	12.9	7.1	7.8
208921_s_at	L12387.1	RacCdc42 guanine exchange factor (GEF) 6	19.2	11.4	20.2	88.6	67.0	37.4	42.4	85.4	6.9	8.9	17.6	21.5	2.6	11.1	12.7	8.4	8.6
209043_at	AF033026.1	sorcin (SOR)	19.9	16.1	39.0	87.1	75.2	66.4	68.7	71.4	13.8	20.0	46.5	8.9	6.3	6.7	4.4	10.6	11.0
		bifunctional ATP																	227
		sulphyaseadenosine																	
		5-phosphosulfate kinase																	30385

Fig. 6M

E. Eosinophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC													Fb	Eo+Ne.S.I.					
			cord blood	MC lung	MC	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo1 (small)	Eo2 (small)	Eo3 (small)	Ne1 (small)	Ne2 (small)	Ne3 (small)	Ne4 (small)			pl CD4	CD8	CD14	CD19	
221345_at	NM_005306.1	GPR	0.1	0.4	0.9	0.6	0.6	7.0	16.6	15.4	10.5	49.7	45.7	23.0	0.8	0.1	0.1	0.7	0.4	0.1	21.742	
212860_at	BG168720	zinc finger, DHHC domain containing 18	2.2	0.8	4.1	3.9	4.0	16.0	17.4	14.8	16.7	59.2	53.9	39.8	1.1	2.4	3.8	2.6	1.5	1.3	6.5842	
211576_s_at	BC003068.1	solute carrier family 19 member 1	1.4	0.1	0.7	1.4	0.7	5.1	5.9	11.5	12.4	19.8	18.7	27.1	1.8	0.9	0.4	2.7	0.5	0.8	4.99	
214321_at	BF440025	nephroblastoma overexpressed gene ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3	1.3	1.0	0.8	0.2	0.7	6.2	7.2	17.0	13.7	4.5	7.6	10.7	11.3	0.1	0.0	0.1	0.1	0.1	4.9823	
218950_at	NM_022481.1		1.4	3.1	2.4	3.7	2.1	15.5	15.9	18.3	15.5	28.0	24.3	15.9	20.6	0.7	0.2	0.8	3.9	0.9	1.0	4.829
205681_at	NM_004049.1	BCL2-related protein A1	0.5	1.9	1.0	3.2	2.4	52.4	40.2	35.9	30.5	46.5	49.2	35.5	33.5	1.5	2.2	1.9	8.3	4.3	0.2	4.7782
203765_at	NM_012198.1	grancalcin	2.0	1.8	4.5	11.7	8.3	27.5	39.8	46.7	34.8	71.6	85.2	80.5	77.9	1.0	1.0	1.2	12.1	3.1	0.5	4.4403
213241_at	AF035307.1	cDNA FLJ36416 fis, clone	5.0	2.4	1.6	1.0	1.0	33.2	37.1	68.7	40.6	63.2	77.8	89.2	80.9	3.0	3.0	2.8	13.5	4.1	7.8	4.2603
221815_at	BE671816	THYMU2011053	1.2	1.4	1.3	0.5	1.6	10.1	8.8	11.2	6.4	5.0	6.2	4.0	3.8	1.6	0.8	0.2	1.4	0.9	0.6	4.1325
214153_at	BE467941	hypothetical protein PRO2831	1.0	0.6	1.0	2.0	3.1	9.1	10.4	18.2	16.6	9.7	9.7	14.5	15.2	0.8	0.9	1.2	0.7	2.3	0.1	4.0797
212821_at	AU147160	homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	0.1	0.1	0.4	1.2	0.9	4.6	2.8	4.7	3.4	4.4	3.5	6.0	7.9	0.4	0.2	0.4	0.3	0.0	0.2	3.727
206723_s_at	AF011466.1	KIAA0599	1.2	1.4	2.1	3.6	2.6	13.7	8.0	19.6	22.3	24.6	17.0	26.1	29.1	0.1	3.6	5.0	3.8	1.9	0.9	3.7119
212360_at	A1916249	Edg4, endothelial differentiation lysophosphatidic acid	1.0	2.0	2.6	5.9	4.6	26.6	18.7	30.2	31.9	78.7	63.1	79.5	91.3	3.4	5.8	6.1	12.6	3.7	5.8	3.5888
218308_at	NM_006342.1	G-protein-coupled receptor, 4	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769
212629_s_at	AK023692.1	adenosine monophosphate deaminase 2 (isoform L)	1.9	0.6	3.1	3.7	5.1	11.8	7.6	17.7	13.8	16.7	23.6	27.0	28.4	1.1	2.1	2.2	4.2	4.2	2.9	3.2963
201739_at	NM_005627.1	transforming, acidic coiled-coil containing protein 3 (TACC3)	30.2	25.2	1.9	18.5	25.4	114.1	116.0	150.9	164.8	60.2	77.1	105.8	156.3	1.1	3.7	0.7	34.6	1.6	18.9	3.2456
209473_at	AV717590	protein kinase C-like 2	1.4	0.6	2.1	1.6	2.0	15.9	22.3	39.5	29.1	14.1	13.7	23.7	13.8	2.6	2.6	1.3	6.5	4.8	0.6	3.0752
209304_x_at	AF087853.1	serum glucocorticoid regulated kinase (SGK)	2.0	0.3	2.7	4.5	3.6	15.5	11.9	16.3	34.4	7.0	12.0	13.5	9.4	0.4	3.1	4.2	4.1	3.7	0.6	3.0295
210666_at	AF050145.1	ectonucleoside triphosphate diphosphohydrolase 1	0.1	0.3	1.3	0.5	1.7	7.1	2.9	3.3	3.8	6.1	5.1	5.2	10.8	0.4	0.1	0.9	0.7	0.4	0.1	3.0005
		growth arrest and DNA damage inducible protein beta (GADD45B)																				
		iduronate 2-sulfatase																				

Fig. 6N

G. Basophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC																		
			cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo1	Eo2	Eo3 (small)	Eo4 (small)	Ne1	Ne2	Ne3 (small)	Ne4 (small)	pl CD4	CD8	CD14	CD19	Fb	Ba+Ne S.I.
218739_at	NM_016006.1	CGI-58 protein	1.8	1.8	7.2	16.3	17.3	2.6	3.3	3.2	2.5	20.7	23.6	21.4	19.3	1.3	1.2	2.9	0.7	1.5	5.81398
219242_at	NM_025180.1	FLJ13386	1.0	0.3	10.1	23.5	18.8	2.4	3.7	4.5	4.2	13.7	14.0	26.1	27.7	0.1	0.5	1.6	0.6	2.5	4.97025
219157_at	NM_007246.1	kelch (Drosophila)-like2	2.4	1.7	4.2	16.2	19.2	3.6	2.5	4.3	3.8	15.5	24.4	24.5	22.5	0.7	2.0	3.0	2.2	1.7	4.61523
206643_at	NM_002108.2	histidine ammonia-lyase	0.1	1.4	8.5	13.7	25.4	0.2	0.6	1.3	0.6	31.4	32.8	61.7	37.0	1.6	0.5	0.1	5.6	0.6	4.57355
213935_at	AF007132.1	clone 23551 mRNA	0.8	0.1	5.0	26.2	26.4	2.4	1.7	2.9	1.2	4.5	6.7	11.2	9.0	0.1	0.1	0.2	2.3	0.5	4.33664
222151_s_at	AK023738.1	FLJ13676 fs	1.0	0.9	4.5	5.5	4.7	1.8	1.7	1.4	1.6	8.4	10.2	8.4	7.6	0.5	0.8	1.3	0.8	1.0	4.14372
207907_at	NM_003807.1	tumor necrosis factor (ligand)	0.1	0.1	3.9	10.4	6.3	1.2	1.5	4.0	4.1	15.8	7.3	15.8	11.5	0.2	0.4	0.1	0.6	0.0	3.89177
202530_at	NM_001315.1	superfamily member 14 (TNFSF 14)	5.0	3.0	28.8	82.2	70.8	4.0	7.1	13.9	11.1	13.6	23.0	25.7	22.3	5.3	2.9	3.5	7.3	2.6	3.8469
217521_at	N54942	mitogen-activated protein kinase 14	0.1	0.1	5.5	18.9	20.9	0.3	0.3	1.6	0.1	19.6	14.5	29.9	18.4	0.4	0.8	0.9	4.3	1.0	3.84207
203693_s_at	NM_001949.2	Hs276590 ESTs	2.5	1.7	4.3	16.2	13.2	2.1	1.9	5.7	3.3	8.8	11.7	13.3	15.4	1.5	1.4	2.5	2.3	1.1	3.7116
203420_at	NM_016255.1	E2F transcription factor 3	2.4	3.3	15.6	31.5	32.4	7.3	6.6	14.3	11.0	37.2	37.2	48.5	50.0	6.1	5.0	9.8	4.5	3.3	3.48188
218308_at	NM_006342.1	autosomal highly conserved protein (AHCP)	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	3.4769
203080_s_at	NM_013450.1	transforming acidic coiled-coil containing protein 3	2.2	2.4	10.4	22.8	22.9	4.9	6.6	10.0	9.5	29.5	30.7	33.5	40.6	1.1	1.7	1.9	4.6	2.3	3.401
219999_at	NM_018621.1	bromodomain adjacent to zinc finger domain, 2B	0.4	0.6	3.9	7.6	8.0	2.0	1.5	3.9	2.7	9.8	6.5	11.7	12.3	0.2	1.3	1.8	2.4	1.7	3.31991
213805_at	AI692428	hypothetical protein PRO2198	0.3	0.1	13.8	11.0	8.7	3.2	3.0	1.4	1.4	19.7	16.7	5.3	7.0	0.7	0.2	0.8	3.3	0.4	3.29317
204669_s_at	NM_007219.2	clone 23551 mRNA	0.9	0.2	4.4	27.9	34.3	2.1	5.9	16.1	14.5	18.8	14.4	60.7	56.1	0.5	0.1	0.1	0.1	0.1	3.18834
215555_at	AK023774.1	ring finger protein 24	0.0	0.4	5.0	4.3	5.8	1.5	1.9	1.5	1.5	7.6	8.2	3.3	3.2	0.9	1.0	1.5	1.5	1.0	3.1591
		FLJ13712 fs																			

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Fig. 60

H. Mast cell and basophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC														MC+Ba.S.I.					
			cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl		CD4	CD8	CD14	CD19	Fb
205624_at	NM_001870.1	carboxypeptidase A3	137.1	91.0	107.6	139.0	173.1	25	1.6	28	1.9	0.1	1.4	2.0	12.4	0.2	1.2	0.2	0.2	0.5	0.5	59.1989
208605_s_at	NM_002529.2	R	8.0	1.2	4.6	9.3	8.1	0.2	0.2	0.0	0.1	0.2	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	34.7309
210258_at	AF030107.1	TRK neurotrophin receptor	62	8.4	5.6	7.1	10.9	0.3	0.1	0.4	0.5	0.5	0.0	0.1	0.3	0.1	0.0	0.0	0.2	0.3	0.0	21.7762
207496_at	NM_000139.1	regulator of G protein signaling (RGS13)	199	24.7	35.4	51.9	45.6	0.9	0.1	0.5	0.3	0.1	0.1	0.5	1.8	1.6	0.5	0.2	0.0	0.3	0.1	21.1783
205857_at	AI269290	R	24.3	27.1	8.1	22.3	25.0	1.3	1.0	0.8	0.9	1.3	0.9	0.5	0.7	0.9	0.4	0.3	0.2	0.3	0.3	20.3301
210358_x_at	BC002557.1	GATA-binding protein 2	184	12.8	55.0	31.7	24.7	2.0	1.6	1.9	1.7	0.9	1.9	1.3	3.7	2.6	0.8	0.8	0.9	0.4	2.7	9.46893
207497_s_at	D10583.1	Fc epsilon R1 beta	10.7	28.6	34.9	12.6	6.8	1.5	1.0	0.8	0.8	1.9	0.9	1.7	1.5	1.7	0.7	0.7	0.1	0.3	0.5	9.39967
203914_x_at	NM_000860.1	15-hydroxyprostaglandin dehydrogenase (PDGH)	63.9	51.4	24.8	36.0	23.3	4.1	4.6	4.6	2.6	1.3	0.9	1.3	1.2	6.0	1.4	1.5	0.4	0.8	0.4	6.14285
219557_s_at	NM_020645.1	chromosome 11 open reading frame 14	7.4	4.2	4.4	7.4	6.6	1.2	1.6	2.0	2.4	0.9	1.9	1.1	2.1	1.1	1.4	1.4	1.5	0.4	1.6	3.38029
204061_at	NM_005044.1	protein kinase, X-linked	6.2	5.2	5.2	12.8	16.9	2.3	2.7	2.5	2.4	0.8	0.4	0.7	1.2	1.9	1.5	2.1	2.5	2.0	0.8	3.26062
202068_s_at	NM_000527.2	R	24.6	16.8	19.3	28.5	13.5	1.6	1.0	1.6	0.9	0.8	2.4	1.5	2.5	2.3	2.1	3.4	3.5	0.8	6.3	3.1679

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Fig. 6P

I. Specific transcripts markers for non-granulocytes.

Probe set	Accession #	Transcripts	MC	cord	Ba1	Ba2	Ba3	EO	EO	EO	EO	Ne	Ne	Ne3	Ne4	pl	CD4	CD8	CD14	CD19	Fb
203547_at	U47924	CD4	4.7	5.5	2.2	1.1	1.2	2.0	1.6	0.4	0.9	0.7	1.1	0.7	0.8	3.5	15.0	0.3	17.6	1.2	0.4
205758_at	AW006735	CD8	1.7	0.5	2.6	2.3	3.2	1.3	1.1	2.2	1.7	0.3	0.5	1.8	0.3	4.2	3.0	76.1	0.8	0.6	0.4
206398_s_at	NM_001770.1	CD19	0.1	0.7	0.7	0.4	0.7	0.8	0.5	0.5	0.2	0.6	1.5	1.1	0.7	4.0	0.0	0.1	0.1	19.1	0.4
211644_x_at	L14458.1	IgGV-Jregion	0.1	0.2	0.1	0.1	0.2	0.2	0.2	0.2	0.3	0.1	0.3	0.2	0.2	3.8	0.1	0.2	0.1	70.9	0.1
201743_at	NM_000591.1	CD14	2.4	18.4	0.3	0.1	0.6	8.8	0.6	1.1	3.2	40.7	49.6	58.7	68.2	2.9	0.4	0.0	97.2	1.1	0.9
203104_at	NM_005211.1	v-fms M-CSF receptor	0.2	3.8	0.6	0.7	0.3	3.0	1.1	1.7	1.5	8.8	8.7	6.3	6.4	5.2	2.8	0.7	42.1	1.4	0.9
209968_s_at	U63041.1	CD56	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.2	0.1	0.0
204627_s_at	M35999.1	CD61 glycoprotein IIIa	9.4	1.7	0.2	0.1	0.3	0.1	0.1	0.1	0.1	0.1	0.4	0.1	0.2	48.3	0.1	0.3	0.1	0.2	0.5
216442_x_at	AK026737.1	fibronectin	1.5	0.3	0.3	0.3	0.2	0.1	1.0	0.3	0.6	0.1	0.1	0.2	0.1	0.3	0.1	1.0	0.3	0.1	92.6

Fig. 6Q

J. Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes.

Probe set	Accession #	Transcripts		MC		Ba 2		Ba 3		Eo		Eo 3		Eo 4		Ne		Ne 3		Ne 4		pI		CD 4		CD 8		CD 14		CD 19		Fb	
		cord	blood	lung	MC	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1 (small)	Eo 2 (small)	Eo 3 (small)	Eo 4 (small)	Ne 1 (small)	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	pI	CD 4	CD 8	CD 14	CD 19	Fb											
AFFX-HSAC07/X00351_3_at	X00351	18534	19383	14638	19383	20922	20922	19151	22019	18638	21153	18568	19406	22302	16589	17569	18295	18782	20805	20661	17542	20399											
AFFX-HSAC07/X00351_M_at	X00351	22898	21777	12940	21777	11533	11533	7608	22560	18785	14861	13431	23106	23373	6861	8019	19368	20362	22761	22294	19087	22757											
AFFX-HSAC07/X00351_5_at	X00351	15642	15838	9516	15838	2927	2927	2066	17186	21061	4861	3771	18772	19768	2165	2193	14887	16381	18218	17583	15063	16795											
AFFX-HUMGAPDH/M33197_3_at	M33197	14906	13632	3640	13632	10477	10477	9332	2649	2844	5498	2605	2549	3186	3586	3538	5929	6429	6098	9756	5180	19674											
AFFX-HUMGAPDH/M33197_M_at	M33197	15891	16852	3218	16852	7587	7587	6963	2382	2565	3720	1838	2194	2796	2312	2154	6182	5931	5921	11464	4344	17013											
AFFX-HUMGAPDH/M33197_5_at	M33197	16298	16701	3479	16701	4559	4559	5110	1827	3121	2127	1168	2492	3476	1636	1355	4655	6826	6260	9905	5636	23350											
The median value of 22283 transcripts		121	1693	853	1122	1109	937	102.1	1273	73.1	87.4	87.3	82.3	152.5	107.1	114.1	183.8																

Abbreviations used in the table A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

Fig. 6R